

## CLAIMS

1           1. A process for altering the host range of  
2       Bacillus toxins which comprises recombining in vitro  
3       the variable region of two or more Bacillus toxin genes.

1           2. A process, according to claim 1, wherein the  
2       Bacillus is a *Bacillus thuringiensis*.

1           3. A process, according to claim 2, wherein  
2 variable regions of Bacillus thuringiensis var.  
3 kurstaki HD-1 and Bacillus thuringiensis var.  
4 kurstaki HD-73 are recombined in vitro to give genes  
5 encoding chimeric toxins having altered host ranges.

1       4. DNA, denoted pEW3, encoding a chimeric toxin  
2 having pesticidal activity, as follows:

		(start)	HD-73)	ATG	GATAACAATC	400
4	CGAACATCAA	TGAATGCATT	CCCTTATAATT	GTTTAAGTAA	CCCTGAAGTA	
5	GAAGTATTAG	GTGGAGAAAAG	AATAGAAACT	GGTTACACCC	CAATCGATAT	500
6	TTCCTTGTG	CTAACGCAAT	TTCTTTGAG	TGAATTGTT	CCCGGTGCTG	
7	GATTGTGTT	AGGACTAGTT	GATATAATAT	GGGGAATT	TGGTCCCTCT	600
8	CAATGGGACG	CATTTCTTGT	ACAAATTGAA	CAGTTAATT	ACCAAAGAAT	
9	AGAAGAATT	GCTAGGAACC	AAGCCATTTC	TAGATTAGAA	GGACTAAGCA	700
10	ATCTTATCA	AATTACGCA	GAATCTTTA	GAGAGTGGGA	AGCAGATCCT	
11	ACTAATCCAG	CATTAAGAGA	AGAGATGCGT	ATTCAATTCA	ATGACATGAA	800
12	CAGTGCCCTT	ACAACCGCTA	TTCCCTCTTT	TGCAGTTCAA	AATTATCAAG	
13	TTCCCTCTTT	ATCAGTATAT	GTTCAGGCTG	CAAATTACA	TTTATCAGTT	900
14	TTGAGAGATG	TTTCAGTGT	TGGACAAAGG	TGGGGATT	ATGCCGCGAC	
15	TATCAATAGT	CGTTATAATG	ATTAACTAG	GCTTATTGGC	AACTATACAG	1000
16	ATTATGCTGT	ACGCTGGTAC	AATACGGGAT	TAGAACGTGT	ATGGGGACCG	
17	GATTCTAGAG	ATTGGGTAAAG	GTATAATCAA	TTTAAAGAG	AATTAACACT	1100
18	AACTGTATT	GATATCGTTG	CTCTGTTCCC	GAATTATGAT	AGTAGAAGAT	
19	ATCCAATTG	AACAGTTCC	CAATTAACAA	GAGAAATT	TACAAACCCA	1200
20	GTATTAGAAA	ATTTGATGG	TAGTTTTCGA	GGCTCGGCTC	AGGGCATAGA	
	AAGAAGTATT	AGGAGTCCAC	ATTGATGGA	TATACTTAAC	AGTATAACCA	1300
	TCTATACGGA	TGCTCATAGG	GGTTATTATT	ATTGGTCAGG	GCATCAAATA	
	ATGGCTTCTC	CTGTAGGGTT	TTCCGGGCCA	GAATTCACTT	TTCCGCTATA	1400
	TGGAACATATG	GGAAATGCAG	CTCCACAAACA	ACGTATTGTT	GCTCAACTAG	
	GTCAGGGCGT	GTATAGAAC	TTATCGTCCA	CTTTATATAG	AAGACCTTT	1500
	AATATAGGGA	TAAATAATCA	ACAACTATCT	GTTCTGACG	GGACAGAATT	
	TGCTTATGGA	ACCTCCTCAA	ATTGCCATC	CGCTGTATAC	AGAAAAAGCG	1600
	GAACGGTAGA	TTCGCTGGAT	GAAATACCGC	CACAGAATAA	CAACGTGCCA	

21 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTCAA TGTTTCGTTC 1700  
 22 AGGCTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)  
 (start HD-1) CCAACGT TTTCTGGCA GCATCGCAGT 1900  
 23 GCTGAATTAA ATAATATAAT TCCCTTCATCA CAAATTACAC AAATAACCTT 1900  
 24 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGGACAG 2000  
 25 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTCA 2000  
 26 ACCTTAAGAG TAAATATTAC TGCAACCATTA TCACAAAGAT ATCGGGTAAG 2100  
 27 AATTGCTAC GCTTCTACTA CAAATTACAA ATTCCATACA TCAATTGACG 2100  
 28 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200  
 29 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTAA 2200  
 30 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300  
 31 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAAGTA 2300  
 32 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400  
 33 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT 2400  
 34 ATCATATTGA TCAAGTATCC AATTAGTTG AGTGTTCATC AGATGAATT 2500  
 35 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG 2500  
 36 ACTTAGTGTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600  
 37 ATAGACAACG AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA 2600  
 38 GGAGGCGATG ACGTATTCAA AGAGAAATTAC GTTACGCTAT TGGGTACCTT 2700  
 39 TGATGAGTGC TATCCAACGT ATTATATATCA AAAAATAGAT GAGTCGAAAT 2700  
 40 TAAAAGCCTA TACCCGTTAT CAATTAAAGAG GGTATATCGA AGATAGTCAA 2800  
 41 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA 2800  
 42 TGTGCCAGGT ACGGGTTCTT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900  
 43 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT 2900  
 44 GACTTAGATT GTTCGTGTAG GGATGAGGAA AAGTGTGCC ATCATTCGCA 3000  
 45 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC 3000  
 46 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
 47 CTAGGGAAATC TAGAAGTTCTT CGAAGAGAGAA CCATTAGTAG GAGAAGCGCT 3100  
 48 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTAAAAAAT 3200  
 49 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT 3200  
 50 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300  
 51 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT 3300  
 52 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400  
 53 GAATTAGAAG GGCSTATTTC CACTGCATTC TCCCTATATG ATGCGAGAAA 3400  
 54 TGTCAATTAA AATGGTGATT TTAATAATGG CTTATCCTGC TGAAACGTGA 3500  
 55 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGTT 3500  
 56 CTTCCGGAAT GGGAAAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600  
 57 TCGTGGCTAT ATCCCTCGTG TCACAGCGTA CAAGGGAGGGA TATGGAGAAG 3600  
 58 GTTGCCTAAC CATTCAATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700  
 59 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA 3700  
 60 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
 61 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC 3800  
 62 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAAATC CTTGTGAATT 3900  
 63 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA 3900  
 64 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
 65 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAAATTAC TCCTTATGGA 4000  
 66 GGAA (end HD-1)

52 and equivalent nucleotide sequences coding for toxin  
53 EW3 with the following amino acid sequence:

54

55 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E  
56 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L  
57 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E  
58 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
59 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V  
60 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q  
61 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
62 Y N T G L E R V W G P D S R D W V R Y N Q F R E L T L T V  
63 L D I V A L F F P N Y D S R R Y P I R T V S Q L T R E I Y T N  
64 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L  
65 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G  
66 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R  
67 T L S S T I L Y R R F F N I G I N N Q Q L S V L D G T E F A Y  
68 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V  
69 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A  
70 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T  
71 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T  
72 L R V N I T A F L S Q R Y A V R I R Y A S T T N L Q F H T S  
73 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G  
74 F T T P F F N F S S N G S S V E T L S A H V F N S G N E V Y I D  
75 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S  
76 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C  
77 L D E K Q E L S E K V / K H A K R L S D E R N L L Q D P N F R  
78 G I N R Q L D R G W R G S T D I T I Q G G G D D V F K E N Y V  
79 T L L G T F D E C Y F T Y L Y Q K I D E S K L K A Y T R Y Q  
80 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T  
81 G S L W P L S A Q S P I G K C G E F N R C A P H L E W N P D

1 5. DNA, denoted pEW4, encoding a chimeric toxin,  
2 having pesticidal activity, as follows:

3 (start HD-1) ATGG ATAACAATCC GAACATCAAT  
4 GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600  
5 TGGAGAAAAGA ATAGAAACTG GTTACACCCC AATCGATATT TCCTTGTCGC  
6 TAACGCAATT TCTTTGAGT GAATTGTTTC CCGGTGCTGG ATTTGTGTTA 700  
7 GGACTAGTTG ATATAATATG GGGAAATTTT GGTCCCTCTC AATGGGACGC  
8 ATTTCCGTAA CAAATTGAAC AGTTAATTAA CCAAAGAATA GAAGAATTG 800  
9 CTAGGAACCA AGCCATTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA  
10 ATTTACGCAAG AATCTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900  
11 ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA  
12 CAACCGCTAT TCCTCTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTA 1000  
13 TCAGTATATG TTCAAGCTGC AAATTTACAT TTATCAGTT TGAGAGATGT  
14 TTCAGTGTGTT GGACAAAGGT GGGGATTGTA TGCCGCGACT ATCAATAGTC 1100  
15 GTTATAATGA TTTAACTAGG CTTATTGGCA ACTATACAGA TTATGCTGTG  
16 CGCTGGTACA ATACGGGATT AGAGCGTGTAA TGGGGACCGG ATTCTAGAGA 1200  
17 TTGGGTAAAGG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG  
18 ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTGCA 1300  
19 ACAGTTTCCC AATTAACAAG AGAAAATTAT ACGAACCCAG TATTAGAAAA  
20 TTTTGATGGT AGTTTTCGTG GAATGGCTCA GAGAATAGAA CAGAATATTA 1400  
21 GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCCT TTATACTGAT  
22 GTGCATAGAG GCTTTAATTAA TTGCTCGGG CATCAAATAA CAGCTTCTCC 1500  
23 TGTAGGGTTT TCAGGACCAAG AATTGCGATT CCCTTTATTT GGGAAATGCGG  
24 GGAATGCGAGC TCCACCCGTA CTTGCTCAT TAACGGTTT GGGGATTTTT 1600  
25 AGAACATTAT CTTCACCTTT ATATAGAAGA ATTATACTTG GTTCAGGCC  
26 AAATAATCAG GAACTGTTTG TCTTGATGAA AACGGAGTT TCTTTGCTT 1700  
27 CCCTAACGAC CAACTTGCT TCCACTATAT ATAGACAAAG GGGTACAGTC  
28 GATTCACTAG ATGTAAATACC GCCACAGGAT AATAGTGTAC CACCTCGTGC 1800  
29 GGGATTTAGC CATCGATTGAA GTCAATTGAA AATGCTGAGC CAAGCAGCTG  
30 GAGCAGTTTA CACCTTGAGA GCTCAACGT (stop HD-1)  
31 (start HD-73) CCT ATGTTCTCTT  
32 GGATACATCG TAGTGTGTGAA TTTAATAATA TAATTGCAATC GGATAGTATT 1800  
33 ACTCAAATCC CTGCAGTGAA GGGAAACTTT CTTTTTAATG GTTCTGTAAT  
34 TTCAAGGACCA GGATTTACTG GTGGGGACTT AGTTAGATTA AATAGTAGTG 1900  
35 GAAATAACAT TCAGAAATAGA GGGTATATTG AAGTTCCAAT TCACTTCCC  
36 TCGACATCTA CCAAGATATCG AGTTCGTGTAA CGGTATGCTT CTGTAACCCC 2000  
37 GATTCACCTC AACGTTAAATT GGGGTAATTC ATCCATTTT TCCAATACAG  
38 TACCAAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTGGT 2100  
39 TATTTGAAA GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG  
40 TGTTAGAAAT TTTAGTGGGA CTGCAGGAGT GATAATAGAC AGATTTGAAT 2200  
41 TTATTCCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG  
42 CAGAAGGCGG TGAATGCGCT GTTACGTCT ACAAAACCAAC TAGGGCTAAA 2300  
43 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT  
44 ATTATCGGA TGAATTGTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400  
45 GTCAAACATG CGAAGCGACT CAGTGTGTAA CGCAATTAC TCCAAGATTC  
46 AAATTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCAGGAAGTA 2500  
47 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAAGA AAATTACGTC  
48 ACACTATCAG GTACCTTGA TGAGTGTCTT CCAACATATT TGTATCAAAA 2600  
49 AATCGATGAA TCAAAATTAA AAGCCTTAC CCGTTATCAA TTAAGAGGGT  
50 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTAAATTG CTACAATGCA 2700  
51 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCCTAT GGCCGCTTTC

36 AGCCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCAGCGC2AC 2800  
37 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGG TGAGAGAAAAG  
38 TGTGCCCATC ATTTCGCATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900  
39 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTAAG ATTAAGACGC  
40 AAGATGGGCA CGCAAGACTA GGGAACTCTAG AGTTTCTCGA AGAGAAACCA 3000  
41 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAATGGAG  
42 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAAGAGG 3100  
43 CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATCAATT  
44 CAAGCGGATA CGAATATTGC CATGATTCAAT GCGGCAGATA AACGTGTTCA 3200  
45 TAGCATTGCA GAAGCTTATC TGCGCTGAGCT GTCGTGATT CGGGGTGTCA  
46 ATGCGGCTAT TTTGAAGAA TTAGAAGGGC GTATTTTCAC TGCAATTCTCC 3300  
47 CTATATGATG CGAGAAAATGT CATTAAAAAT GGTGATTTA ATAATGGCTT  
48 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400  
49 AACGTTCGGT CCTTGTTGTT CGGGAAATGGG AAGCAGAAAGT GTCACAAGAA  
50 GTTCGTGTCT GTCCGGGTG GGGCTATATC CTTCGTGTCA CAGCGTACAA 3500  
51 GGAGGGATAT GGAGAAGGTT GCGTAAACCAT TCATGAGATC GAGAACAAATA  
52 CAGACGAACT GAAGTTTAGC AACTGCGTAG AAGAGGAAAT CTATCCAAAT 3600  
53 AACACGGTAA CGTGTAAATGA TTATACTGTA AATCAAGAAG AATACGGAGG  
54 TGCCTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAAG 3700  
55 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA  
56 GAGAATCCTT GTGAATTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800  
57 AGTTGGTTAT GTGACAAAAG AATTAGAATA CTTCCCAGAA ACCGATAAGG  
58 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTATCGT GGACAGCGTG 3900  
59 GAATTACTCC TTATGGAGGA A (end HD-73)

and equivalent nucleotide sequences coding for toxin  
EW4 with the following amino acid sequence:

54 M D N N F N I N E C I P Y N C L S N P E V E V L G G E R I E  
55 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L  
56 V D I I W G I F G P S Q W D A F P V Q I E Q L I N Q R I E E  
57 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
58 P T N P A L R E E M R I Q F N D M N S A L T T A I P L L A V  
59 Q N Y Q V F L L S V Y V Q A A N L H L S V L R D V S V F G Q  
60 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
61 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V  
62 L D I V A L F S N Y D S R R Y P I R T V S Q L T R E I Y T N  
63 P V L E N F D G S F R G M A Q R I E Q N I R Q P H L M D I L  
64 N S I T I Y T D V H R G F N Y W S G H Q I T A S P V G F S G  
65 P E F A F P L F G N A G N A A P P V L V S L T G L G I F R T  
66 L S S F L Y R R I I L G S G P N N Q E L F V L D G T E F S F  
67 A S L T T N L P S T I Y R Q R G T V D S L D V I P P Q D N S  
68 V P P F R A G F S H R L S H V T M L S Q A A G A V Y T L R A Q  
69 R P M F S W I H R S A E F N N I I A S D S I T Q I P A V K G  
70 N F L F N G S V I S G P G F T G S D L V R L N S S G N N I Q  
71 N R G Y I E V P I H F F P S T S T R Y R V R V R Y A S V T P I  
72 H L N V N W G N S S I F S N T V F A T A T S L D N L Q S S D  
73 F G Y F E S A N A F T S S L G N I V G V R N F S G T A G V I  
74 I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F  
75 T S T N Q L G L K T N V T D Y H I D Q V S N L V T Y L S D E  
76 F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N  
77 F K D I N R Q P E R G W G G S T G I T I Q G G D D V F K E N  
78 Y V T L S G T F D E C Y P T Y L Y Q K I D E S K L K A F T R  
79 Y Q L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P  
80 G T G S L W P E S A Q S P I G K C G E F N R C A P H L E W N  
P D L D C S C R D G E K C A H H S H H F S L D I D V G C T D  
L N E D L G V W V I F K I K T Q D G H A R L G N L E F L E E  
K P L V G E A L A R V K R A E K K W R D K R E K L E W E T N  
I V Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M  
I H A A D K R V H S I R E A Y L P E L S V I P G V N A A I F  
E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S  
C W N V K G H V D V E E Q N N Q R S V L V V P E W E A E V S  
Q E V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H  
E I E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y  
T V N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S  
V Y E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V  
G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D  
S V E L L L M E E.

1       6. DNA, denoted pACB-1, encoding a chimeric toxin,  
2 having pesticidal activity, as follows:

3 (start HD-73) ATG GATAACAATC 400  
 4 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA  
 5 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTTACACCC CAATCGATAT 500  
 6 TTCCCTGTCG CTAACGCAAT TTCTTTGAG TGAATTGTT CCCGGTGCCTG  
 7 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTC TGGTCCCTCT 600  
 8 CAATGGGACG CATTCTTGT ACAAAATTGAA CAGTTAATTA ACCAAAGAAT  
 9 AGAAGAATTG GCTAGGAACC AAGCCATTTC TAGATTAGAA GGACTAAGCA 700  
 10 ATCTTATCA AATTACGCA GAATCTTTA GAGAGTGGGA AGCAGATCCT  
 11 ACTAATCCAG CATTAAAGAGA AGAGATGCCT ATTCAATTCA ATGACATGAA 800  
 12 CAGTGCCCTT ACAACCGCTA TTCCCTTTTG TGCAGTTCAA AATTATCAAG  
 13 TTCCCTTTT ATCAGTATAT GTTCAAGCTG CAAATTACAA TTTATCAGTT 900  
 14 TTGAGAGATG TTTCAGTGTG TGGACAAAGG TGGGGATTG ATGCCGCGAC  
 15 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATGGC AACTATACAG 1000  
 16 ATTATGCTGT ACGCTGGTAC AATAACGGGAT TAGAACGCTG ATGGGGACCG  
 17 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAAACACT 1100  
 18 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT  
 19 ATCCAATTG AACAGTTCC CAATTAACAA GAGAAATTAA TACAAACCCA 1200  
 20 GTATTAGAAA ATTTTGATGG TAGTTTTCGA GGCTCGGCTC AGGGCATAGA  
 21 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300  
 22 TCTATACGGA TGCTCATAGG GGTTATTATT ATTGGTCAGG GCATCAAATA  
 23 ATGGCTTCTC CTGTAGGGTT TTGGGGCCA GAATTCACTT TTCCGCTATA 1400  
 24 TGGAACTATG GGAAATGCAG CTCAACAAAC ACGTATTGTT GCTCAACTAG  
 25 GTCAGGGCGT GTATAGAACAA TTATCGTCZA CTTTATATAG AAGACCTTT 1500  
 26 AATATAAGGGA TAAATAATCA ACAAATATCT GTTCTTGACG GGACAGAATT  
 27 TGCTTATGGA ACCTCCTCAA ATTGCCATC CGCTGTATAC AGAAAAAGCG 1600  
 28 GAACGGTAGA TTGCTGAAT GAAATACCGC CACAGAATAA CAACGTGCCA  
 29 CCTAGGCAAG AATTAGTCA TOGATTAAGC CATGTTCAA TGTTTGTTC 1700  
 30 AGGCTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)  
 31 (start HD-11) CCAACGT TTTCTGGCA GCATCGCAGT 1900  
 32 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTT  
 33 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAAG 2000  
 34 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTTC  
 35 ACCTTAAGAG TAAATATTAC TGCAACCATTA TCACAAAGAT ATCGGGTAAG 2100  
 36 AATTGCTAC GCTTCTACTA CAAATTTACA ATTCCATACAC TCAATTGACG  
 37 GAAGACCTAT TAATCAGGGT AATTTCAG CAACTATGAG TAACTGGGAGT 2200  
 38 AATTTACAGT CCGGAAGCTT TAGGACTGTA GTTTTACTA CTCCGTTAA  
 39 CTTTCAAT GGATCAAGTG TATTACGTT AAGTGCTCAT GTCTTCATT 2300  
 40 CAGGCAATGA AGTTTATATA GATCGAATTG AATTGTTCC GGCAAGAGTA  
 41 ACCTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400  
 42 GCTGTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT  
 43 ATCATATTGA TCAAGTATCC AATTAGTGT AGTGTTCATC AGATGAATT 2500  
 44 TGTCGGATG AAAAACAAAGA ATTGTCGAG AAGTCAAAC ATGCGAAGCG  
 45 ACTTAGTGT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600  
 46 ATAGACAATC AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA  
 47 GGAGGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700  
 48 TGATGAGTGC TATCCAACTGT ATTATATCA AAAAATAGAT GAGTCGAAAT  
 49 TAAAAGCCTA TACCCGTTAT CAATTAAAGAG GGTATATCGA AGATAGTCAA 2800  
 50 GACTTAGAAA TCTATTAAAT TCGCTACAAAT GCAAAACATG AAACAGTAAA  
 51 TGTGCCAGGT ACGGGTTCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900  
 52 GAAAGTGTGG AGAGCCGAAT CGATCGCGC CACACCTTGA ATGGAATCCT  
 53 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCA ATCATTGCA 3000  
 54 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC

55 TAGGTGTATG GGTGATCTT AAGATTAAGA CGCAAGATGG GCAAGCAAGA 3100  
 56 CTTAGGGAATC TAGAGTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCCT  
 57 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTAAAAAAT 3200  
 58 TGGAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT  
 59 GCTTTATTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACAAATAT 3300  
 60 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT  
 61 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400  
 62 GAATTAGAAG GCGTATTTC CACTGCATT CTCCTATATG ATGCGAGAAA  
 63 TGTCATTAAG AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500  
 64 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCCCTGTT  
 65 CTTCCGGAAT GGGAAAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600  
 66 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG  
 67 GTTGCCTAAC CATTCACTGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700  
 68 AGCAACTGCG TAGAAGAGGAA AATCTATCCA AATAAACACGG TAACGTGTAA  
 69 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
 70 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGGTGATTA TGCCTCAGTC  
 71 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAAATC CTTGTGAATT 3900  
 72 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
 73 AAGAATTAGA ATACTTCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
 74 GAAACGGAAG GAACATTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA  
 75 GGAA (end HD-1)

76 and equivalent nucleotide sequences coding for toxin  
 77 ACB-1 with the following amino acid sequence:

78 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E  
 79 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L  
 80 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E  
 81 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
 82 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V  
 83 Q N Y Q V P F L L S V Y V Q A A N L H L S V L R D V S V F G Q  
 84 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
 85 Y N T G L E R V W G F D S R D W V R Y N Q F R R E L T L T V  
 86 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N  
 87 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L  
 88 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G  
 89 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R  
 90 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y  
 91 G T S S N L P S A V Y R K S G T V D S L N E I F P Q N N N V  
 92 P P R Q E F S H R L S H V S M F R S G F S N S S V S I I R A  
 93 P T F S W Q H R S A E F N N I I F S S Q I T Q I P L T K S T  
 94 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T  
 95 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S  
 96 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G

97 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D  
 98 R I E F V P A E V T F E A E Y D L E R A Q K A V N E V F T S  
 99 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C  
 100 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R  
 101 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V  
 102 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q  
 103 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T  
 104 G S L W P L S A Q S P I G K C G E F N R C A P H L E W N P D  
 105 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N  
 106 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P  
 107 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V  
 108 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H  
 109 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E  
 110 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W  
 111 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E  
 112 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I  
 113 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V  
 114 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y  
 115 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y  
 116 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V  
 117 E L L L M E E.

1 7. DNA, denoted pSYW1, encoding a chimeric toxin,  
 2 having pesticidal activity, as follows:

3 (start HD-73) ATG GATAACAATC 400  
 4 CGAACATCAA TGAATGCAATT CCTTATAATT GTTTAAGTAA CCTGAAAGTA  
 5 GAAGTATTAG GTGGAGAAAG AATAGAAAATC GTTACACCCC CAATCGATAT 500  
 6 TTCCCTTGTCG CTAACGCAAT TTCTTTGAG TGAATTGTT CCCGGTGCTG  
 7 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600  
 8 CAATGGGACG CATTCTTGT ACAAAATTGAA CAGTTAATTA ACCAAAGAAT  
 9 AGAAGAATTC GCTAGGAACC AAGCCATTTC TAGATTAGAA GGACTAAGCA 700  
 10 ATCTTTATCA AATTTACGCA GAATCTTTA GAGAGTGGGA AGCAGATCCT  
 11 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800  
 12 CAGTGCCTT ACAACCGCTA TTCCCTTTT TGCAGTTCAA AATTATCAAG  
 13 TTCCCTTTT ATCACTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900  
 14 TTGAGAGATG TTTCAGTGTG TGGACAAAGG TGGGGATTTG ATGCCGCGAC  
 15 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000  
 16 ATTATGCTGT ACGCTGGTAC AATACTGGGAT TAGAACGTGT ATGGGGACCG  
 17 GATTGTAGAG ATTGGGTAAG GTATAATCAA TTAGAGAG AATTAACACT 1100  
 18 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT  
 19 ATCCAATTG AACAGTTTCC CAATTAACAA GAGAAATTAA TACAAACCCA 1200  
 20 GTATTAGAAA ATTGATGG TAGTTTCGA GGCTCGGCTC AGGGCATAGA  
 21 AGGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300  
 22 TCTATACGGA TGCTCATAAA GGGGAATATT ATTGGTCAGG GCATCAAATA  
 23 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400  
 24 TGGAACCTATG GGAATGCAAG CTCCACAAACA ACGTATTGTT GCTCAACTAG  
 25 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500  
 26 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT

27 TGCTTATGGA ACCTCCTCAA ATTGCCATC CGCTGTATAC AGAAAAAAGCG 1600  
 28 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCGA  
 29 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTCAA TGTTTCGTTC 1700  
 30 AGGCTTCTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-7B)  
 31 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900  
 32 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT  
 33 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTGCGT AAAGGACCAG 2000  
 34 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CGAGATTTC  
 35 ACCTTAAGAG TAAATATTAC TGCAACCATTA TCACAAAGAT ATCGGGTAAG 2100  
 36 AATTGCTACTA GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG  
 37 GAAGACCTAT TAATCAGGGT AATTTCAG CAACTATGAG TAGTGGGAGT 2200  
 38 AATTACAGT CCGGAAGCTT TAGGACTGTA GGTTTACTA CTCCGTTAA  
 39 CTTTCAAAT GGATCAAGTG TATTACGTT AAGTGCTCAT GTCTTCATT 2300  
 40 CAGGCAATGA AGTTTATATA GATCGAATTG AATTGTTCC GGCAGAAGTA  
 41 ACCTTGAGG CAGAATATGA TTTAGAAAGA GCAGAAAAGG CGGTGAATGA 2400  
 42 GCTGTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT  
 43 ATCATATTGA TCAAGTATCC AATTAGTTG ATGTGTTTATC AGATGAATT 2500  
 44 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG  
 45 ACTTAGTGTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600  
 46 ATAGACAACG AGACCGTGCG TGGAGAGGAA GTACGGATAT TACCATCCAA  
 47 GGAGGCAGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700  
 48 TGATGAGTGC TATCCAACGT ATTATATCA AAAAATAGAT GAGTCGAAAT  
 49 TAAAAGCCTA TACCCGTTAT CAATTAAAGAG GGTATAATGA AGATAGTC 2800  
 50 GACTTAGAAA TCTATTTAAT TCGGTACAAT GCAGAACATG AAACAGTAAA  
 51 TGTGCCAGGT ACGGGTTCTT TATGCCGCTT TCAGCCCAA AGTCCAATCG 2900  
 52 GAAAGTGTGG AGAGCCGAAAT CGATGCGCGC CACACCTTGA ATGGAATCCT  
 53 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCC ATCATTGCA 3000  
 54 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC  
 55 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
 56 CTAGGGAAATC TAGAGTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT  
 57 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTAAAAAAT 3200  
 58 TGGAAATGGGA AACAAATATC GTTATAAAG AGGCAAAAGA ATCTGTAGAT  
 59 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300  
 60 TGCCATGATT CATGCCGCGAG ATAAACGTGT TCATAGCATT CGAGAAAGCTT  
 61 ATCTGCCTGA GGTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400  
 62 GAATTAGAAG GCGTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA  
 63 TGTCAATTAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500  
 64 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTG GGTCTTGT  
 65 CTTCCGGAAT GGGAAAGCAGA AGTGTACCAA GAAGTTCGTG TCTGTCCGGG 3600  
 66 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGAA TATGGAGAAAG  
 67 GTTGCCTAAC CATTCAATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700  
 68 AGCAACTCGG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA  
 69 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
 70 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC  
 71 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAACATC CTTCGTAAATT 3900  
 72 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
 73 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
 74 GAAACGGAAG GAACATTAT CGTGGACACGC GTGGAAATTAC TCCTTATGGA  
 75 GGAA (end HD-1)

76 and equivalent nucleotide sequences coding for toxin  
77 SYW1 with the following amino acid sequence:

78 M D N N P N I N E C I P Y N C L S N P E V E V L G Q E R I E  
79 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L  
80 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E  
81 F A R N Q A I S R L E G L S N L Y Q I Y A E S P R E W E A D  
82 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V  
83 Q N Y Q V P L L S V Y V V Q A A N L H L S V L R D V S V F G Q  
84 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
85 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V  
86 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N  
87 P V L E N F D G S F R G S A Q G I E G S I R S P H L M D I L  
88 N S I T I Y T D A H K G E Y Y W S G H Q I M A S P V G F S G  
89 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R  
90 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y  
91 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V  
92 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A  
93 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T  
94 N L G S G T S V V K G P G F T S G D I L R R T S P G Q I S T  
95 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S  
96 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G  
97 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D  
98 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S  
99 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C  
100 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R  
101 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V  
102 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q  
103 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T  
104 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D  
105 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N  
106 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P  
107 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V  
108 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H  
109 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E  
110 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W  
111 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E  
112 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I  
113 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V  
114 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y  
115 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L R V G Y  
116 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V  
117 E L L L M E E .

1        8. A chimeric toxin, EW3, having pesticidal  
2        activity, having the following amino acid sequence:

3        M D N N P N I N E C I P Y N C I S N P E V E V L G G E R I E  
4        T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L  
5        V D I I W G I F G P S Q W D A F L V O I E Q L I N Q R I E E  
6        F A R N Q A I S R L E G L S N L Y Q I Y A E S P R E W E A D  
7        P T N P A L R E E M R I Q F N D M M N S A L T T A I P L F A V  
8        Q N Y Q V P F L L S V Y V Q A A N L H L S V L R D V S V F G Q  
9        R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
10        Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V  
11        L D I V A L F F P N Y D S R R Y P I R T V S Q L T R E I Y T N  
12        P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L  
13        N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G  
14        P E F T F F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R  
15        T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y  
16        G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V  
17        P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A  
18        P T F S W Q H R S A E F N N I I F S S Q I T Q I P L T K S T  
19        N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T  
20        L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S  
21        I D G R P I N Q G N F S A T M S S S S N L Q S G S F R T V G  
22        F T T P F N F S N G S S V E T L S A H V F N S G N E V Y I D  
23        R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S  
24        S N Q I G L K T D V T D H I D Q V S N L V E C L S D E F C  
25        L D E K Q E L L S E K V K H A K R L S D E R N L L Q D P N F R  
26        G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V  
27        T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q  
28        L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T  
29        G S L W P L S A Q S P I G K C G E P N R C A F H L E W N P D  
30        L D C S O R D G E K C A H H S H H F S L D I D V G C T D L N  
31        E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P  
32        L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V  
33        Y K E A K E S V D A L F V N S Q Y D O L Q A D T N I A M I H  
34        A A D K R V H S I R E A Y L P E L S V I F G V N A A I F E E  
35        L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W  
36        N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E  
37        V R V C F G R G Y I L R V T A Y K E G Y G E G C V T I H E I  
38        E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V  
39        N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y  
40        E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y  
41        V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V  
42        E L L L M E E

43        and muteins thercof which do not alter the protein  
44        secondary structure.

1       9. A chimeric toxin, EW4, having pesticidal  
2       activity, having the following amino acid sequence:

3       M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E  
4       T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L  
5       V D I I W G I F G P S Q W D A F F P V Q I E Q L I N Q R I E E  
6       F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
7       P T N P A L R E E M R I Q F N D M N S A L T T A I P L L A V  
8       Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q  
9       R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
10      Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V  
11      L D I V A L F S N Y D S R R Y P I R T V S Q L T R E I Y T N  
12      P V L E N F D G S F R G M A Q R I E Q N I R Q P H L M D I L  
13      N S I T I Y T D V H R G F N Y W S G H Q I T A S P V G F S G  
14      P E F A F F P L F G N A G N A A F P P V L V S L T G L G I F R T  
15      L S S P L Y R R I I I L G S G P N N Q E L F V L D G T E F S F  
16      A S L T T N L P S T I Y R Q R G T V D S L D V I P P Q D N S  
17      V P P R A G F S H R L S H Y T M L S Q A A G A V Y T L R A Q  
18      R P M F S W I H R S A E F N N I I A S D S I T Q I P A V K G  
18      N F L F N G S V I S G P G R T G G D L V R L N S S G N N I Q  
20      N R G Y I E V P I H F P S T S T R Y R V R V R Y A S V T P I  
21      H L N V N W G N S S I F S M T V P A T A T S L D N L Q S S D  
22      F G Y F E S A N A F T S S L G N I V S V R N F S G T A G V I  
23      I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F  
24      T S T N Q L G L K T N V T D Y H I D Q V S N L V T Y L S D E  
25      F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N  
26      F K D I N R Q P E R G W G G S T G I T I Q G G D D V F K E N  
27      Y V T L S G T F D E C Y F T Y L Y Q K I D E S K L K A F T R  
28      Y Q L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P  
29      G T G S L W P L S A Q S P I G K C G E P N R C A P H L E W N  
30      P D L D C S C R D G E K C A H H S H H F S L D I D V G C T D  
31      L N E D L G V W V I F K I K T Q D G H A R L G N L E F L E E  
32      K P L V G E A L A R V K R A E K K W R D K R E K L E W E T N  
33      I V Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M  
34      I H A A D K R V H S I R E A Y L P E L S V I P G V N A A I F  
35      E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S  
36      C W N V K G H V D V E E Q N N Q R S V L V V P E W E A E V S  
37      Q E V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H  
38      E I E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y  
39      T V N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S  
40      V Y E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V  
41      G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D  
42      S V E L L L M E E

43      and muteins thereof which do not alter the protein  
44      secondary structure.

1       10. A chimeric toxin, ACB-1, having pesticidal  
2       activity, having the following amino acid sequence:

3       M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E  
4       T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L  
5       V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E  
6       F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
7       P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V  
8       Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q  
9       R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
10       Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V  
11       L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N  
12       P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L  
13       N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G  
14       P E F T F F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R  
15       T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y  
16       G T S S N L P S A V Y R K S G T V D S L N E I P P Q N N N V  
17       P P R Q E F S H R L S H V S M F R S G F S N S S V S I I R A  
18       P T F S W Q H R S A E F N N I I F S S Q I T Q I P L T K S T  
19       N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T  
20       L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S  
21       I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G  
22       F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D  
23       R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S  
24       S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C  
25       L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R  
26       G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V  
27       T L L G T F D E C Y P T Y Y Q K I D E S K L K A Y T R Y Q  
28       L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T  
29       G S L W P L S A Q S P I G K C G E F N R C A P H L E W N P D  
30       L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N  
31       E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P  
32       L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V  
33       Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H  
34       A A D K R V H S I R E A Y L P E L S V I F G V N A A I F E E  
35       L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W  
36       N V K G H V D V E E Q N N N Q R S V L V L P E W E A E V S Q E  
37       V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I  
38       E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V  
39       N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y  
40       E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y  
41       V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V  
42       E L L M E E

43       and muteins thereof which do not alter the protein  
44       secondary structure.

1 11. A chimeric toxin, SYW1, having pesticidal  
2 activity, having the following amino acid sequence:

3 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E  
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L  
5 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E  
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V  
8 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q  
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
10 Y N T G L E R V W G P D S R D W V R Y N Q F R E L T L T V  
11 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N  
12 P V L E N F D G S F R G S A Q G I E G S I R S P H L M D I L  
13 N S I T I Y T D A H K G E Y Y W S G H Q I M A S P V G F S G  
14 P E F T F F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R  
15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y  
16 G T S S N L P S A V Y R K S G T V D S L D E I P P P Q N N N V  
17 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A  
18 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T  
19 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T  
20 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S  
21 I D G R R P I N Q G N F S A T M S S G S N L Q S G S F R T V G  
22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D  
23 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S  
24 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C  
25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R  
26 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V  
27 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q  
28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T  
29 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D  
30 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N  
31 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P  
32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V  
33 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H  
34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E  
35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W  
36 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E  
37 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I  
38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V  
39 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y  
40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y  
41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V  
42 E L L L M E E

43 and muteins thereof which do not alter the protein  
44 secondary structure.

1           12. A pesticidal composition comprising pesti-  
2       cide-containing substantially intact cells having  
3       prolonged pesticidal activity when applied to the  
4       environment of a target pest, wherein said pesticide,  
5       is a chimeric toxin, is intracellular and is produced  
6       as a result of expression of a heterologous gene  
7       encoding said chimeric toxin in said cell.

1           13. A pesticidal composition according to claim 12,  
2       wherein said cells are killed under protease deacti-  
3       vating or cell wall strengthening conditions, while  
4       retaining pesticidal activity.

1           14. A pesticidal composition, according to claim 12,  
2       wherein said cells are prokaryotes selected from the  
3       group consisting of Enterobacteriaceae, Bacillaceae,  
4       Rhizobiaceae, Spirillaceae, Lactobacillaceae, Pseudo-  
5       monadaceae, Azotobacteraceae, and Nitrobacteraceae; or  
6       lower eukaryotes selected from the group consisting  
7       of Phycomycetes, Ascomycetes, and Basidiomycetes.

1           15. A pesticidal composition, according to claim 14,  
2       wherein said prokaryote is a Bacillus specie selected  
3       from a pesticide-producing strain of Bacillus thurin-  
4       giensis, consisting of B. thuringiensis M-7, B. thurin-  
5       giensis var. kurstaki, B. thuringiensis var. finitimus,  
6       B. thuringiensis var. alesti, B. thuringiensis var.  
7       sotto, B. thuringiensis var. dendrolymus, B. thurin-  
8       giensis var. kenyae, B. thuringiensis var. galleriae,  
9       B. thuringiensis var. canadensis, B. thuringiensis var.  
10      entomocidus, B. thuringiensis var. subtoxicus, B.  
11      thuringiensis var. aizawai, B. thuringiensis var. morri-  
12      soni, B. thuringiensis var. ostriniae, B. thuringiensis  
13      var. tolworthi, B. thuringiensis var. darmstadiensis,

14       B. thuringiensis var. toumanoffi, B. thuringiensis var.  
15       kyushuensis, B. thuringiensis var. thompsoni, B.  
16       thuringiensis var. pakistani, B. thuringiensis var.  
17       israelensis, B. thuringiensis var. indiana, B. thurin-  
18       giensis var. dakota, B. thuringiensis var. tohokuensis,  
19       B. thuringiensis var. kumanotoensis, B. thuringiensis  
20       var. tochigiensis, B. thuringiensis var. colmeri,  
21       B. thuringiensis var. wuhanensis, B. thuringiensis  
22       var. tenebrionis, B. thuringiensis var. thuringiensis,  
23       and other Bacillus species selected from B. cereus, B.  
24       moritai, B. popilliae, B. lentimorbus, and B. sphaericus.

1       16. A method of protecting plants against pests  
2       which comprises applying to said plants an effective  
3       amount of a pesticidal composition comprising pesti-  
4       cide-containing substantially intact unicellular  
5       microorganisms, wherein said pesticide is a chimeric  
6       toxin, is intracellular, and is produced as a result  
7       of expression of a heterologous gene encoding said  
8       chimeric toxin in said microorganism, and said micro-  
9       organism is treated under conditions which prolong  
10      the pesticidal activity when said composition is applied  
11      to the environment of a target pest.

1       17. A method according to claim 16, wherein said  
2       microorganisms are prokaryotes selected from the  
3       group consisting of Enterobacteriaceae, Bacillaceae,  
4       Rhizobiaceae, Spirillaceae, Lactobacillaceae, Pseudo-  
5       monadaceae, Azotobacteraceae, and Nitrobacteraceae; or  
6       lower eukaryotes, selected from the group consisting  
7       of Phycomycetes, Ascomycetes, and Basidiomycetes.

1           18. A method according to claim 16, wherein said  
2       unicellular microorganisms are killed under protease  
3       deactivating or cell wall strengthening conditions,  
4       while retaining pesticidal activity.

1           19. Substantially intact unicellular microorganism  
2        cells containing an intracellular chimeric toxin, which  
3        toxin is a result of expression of a heterologous  
4        gene encoding said chimeric toxin, wherein said cells  
5        are killed under protease deactivating or cell wall  
6        strengthening conditions, while retaining pesticidal  
7        activity when said cell is applied to the environment  
8        of a target pest.

1           21. A pesticidal composition, according to claim  
2        12, wherein said gene, denoted pEW3, encoding a  
3        chimeric toxin, is as follows:

		(start	HD-73)		ATG	GATAACAATC	400
4	CGAACATCAA	TGAATGCATT	CCTTATAATT	GTTTAAGTAA	CCCTGAAGTA		
5	GAAGTATTAG	GTGGAGAAAG	AATAGAAAATC	GGTTACACCC	CAATCGATAT	500	
6	TTCCCTGTG	CTAACGCAAT	TTCTTTGAG	TGAATTGTT	CCCGGTGCTG		
7	GATTTGTGTT	AGGACTAGTT	GATATAATAT	GGGGAATTTC	TGGTCCCTCT	600	
8	CAATGGGACG	CATTCTGTG	ACAAATTGAA	CAGTTAATT	ACCAAAGAAT		
9	AGAAGAATTG	GCTAGGAAACC	AAGCCATTTC	TAGATTAGAA	GGACTAAGCA	700	
10	ATCTTATCA	AATTTACGCA	GAATCTTTA	GAGAGTGGGA	AGCAGATCCT		
11	ACTAATCCAG	CATTAAGAGA	AGAGATGCGT	ATTCAATTCA	ATGACATGAA	800	
12	CAGTGCCTT	ACAACCGCTA	TTCCCTTTT	TGCAGTTCAA	AATTATCAAG		
13	TTCCCTTTT	ATCAGTATAT	GTTCAGCTG	CAAATTACAA	TTTATCAGTT	900	
14	TTGAGAGATG	TTTCAGTGT	TGGACAAAGG	TGGGGATTTG	ATGCCGCGAC		
15	TATCAATAGT	CGTTATAATG	ATTTAACATG	GCTTATTGGC	AACTATACAG	1000	
	ATTATGCTGT	ACGCTGGTAC	AATAACGGGAT	TAGAACGTGT	ATGGGGACCG		
	GATTCTAGAG	ATTGGGTAAG	GTATAATCAA	TTTAAAGAG	AATTAAACACT	1100	
	AACTGTATTA	GATATCGTTG	CTCTGTTCCC	GAATTATGAT	AGTAGAAAGAT		
	ATCCAATTG	AACAGTTTCC	CAATTAACAA	GAGAAATTTC	TACAAAACCCA	1200	
	GTATTAGAAA	ATTTTGATGG	TAGTTTTCGA	GGCTCGGCTC	AGGGCATAGA		

16 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300  
 17 TCTATACGGA TGCTCATAGG GGTTTATTATT ATTGGTCAGG GCATCAAATA  
 18 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400  
 19 TGGAACATATG GGAAATGCAG CTCCACAAACA ACGTATTGTT GCTCAACTAG  
 20 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTT 1500  
 21 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT  
 22 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600  
 23 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA  
 24 CCTAGGCAG GATTTAGTCA TCGATTAAGC CATGTTCAA TGTTTCGTT 1700  
 25 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end HD-73)  
 26 (start HD-1) CCAACGT TTTCTGGCA GCATCGCAGT 1900  
 27 GCTGAATTAA ATAATATAAT TCCCTCATCA CAAATTACAC AAATACCTT  
 28 AACAAAATCT ACTAATCTT GCTCTGGAAC TTCTGTCGTT AAAGGACAG 2000  
 29 GATTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTG CAGATTCA  
 30 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100  
 31 AATTGCTAC GCTTCTACTA CAAATTACA ATTCCATACA TCAATTGACG  
 32 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200  
 33 AATTACAGT CCGGAAGCTT TAGGACTGTA GGTTTACTA CTCCGTTAA  
 34 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300  
 35 CAGGCAATGA AGTTTATATA GATCGAATTG AATTGTTCC GGCAGAAGTA  
 36 ACCTTGAGG CAGAATATGA TTAGAAAGA GCACAAAAGG CGGTGAATGA 2400  
 37 GCTGTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT  
 38 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATT 2500  
 39 TGTCTGGATG AAAAACAAAGA ATTGTCGAG AAAGTCAAAC ATGCGAAGCG  
 40 ACTTAGTGTG GAGCGGAATT TACTCAAGA TCCAAATTC AGAGGGATCA 2600  
 41 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA  
 42 GGAGGCCATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700  
 43 TGATGAGTGC TATCCAACGT ATTATATCA AAAAATAGAT GAGTCGAAAT  
 44 TAAAAGCCTA TACCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800  
 45 GACTTAGAAA TCTATTTAAT TCGCTACAAAT GCAAAACATG AAACAGTAAA  
 46 TGTGCCAGGT ACGGGTTCCCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900  
 47 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTGAA ATGGAATCCT  
 48 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCC ATCATTGCA 3000  
 49 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC  
 50 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
 51 CTAGGGAATC TAGAGTTCT CGAAGAGAAAA CCATTAGTAG GAGAAGCGCT  
 52 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTAAAAAT 3200  
 53 TGGAATGGGA AACAAATATC GTTATAAAG AGGCAAAAGA ATCTGTAGAT  
 54 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300  
 55 TGCCATGATT CATGCGCGAG ATAAACGTGT TCATAGCATT CGAGAACCTT  
 56 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400  
 57 GAATTAGAAG GGC GTTATTT CACTGCATTC TCCCTATATG ATGCAGAGAAA  
 58 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500  
 59 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCTTGTT  
 60 CTTCCGGAAT GGGAAAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600  
 61 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGAA TATGGAGAAG  
 62 GTTGCGTAAC CATTCAATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700  
 63 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA  
 64 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
 65 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCGTCAGTC  
 66 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900  
 67 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
 68 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
 69 GAAACGGGAAG GAACATTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA  
 70 GGAA (end HD-1)

52 and equivalent nucleotide sequences coding for toxin  
53 EW3 with the following amino acid sequence:

54 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E  
55 T G Y T P I D I S L S L T Q F L L S E F V P G A S F V L G L  
56 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E  
57 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
58 P T N P A L R E E M R I Q F N D M N S A L T A I P L F A V  
59 Q N Y Q V F L L S V Y V Q A A N L H L S V L R D V S V F G Q  
60 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
61 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V  
62 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N  
63 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L  
64 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G  
65 P E F T F F L Y G T M G N A A F Q Q R I V A Q L G Q G V Y R  
66 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y  
67 G T S S N L F S A V Y R K S G T V D S L D E I P P Q N N N V  
68 P P R Q G F F S H R L S H V S M F R S G F S N S S V S I I R A  
69 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T  
70 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T  
71 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S  
72 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G  
73 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D  
74 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S  
75 S N Q I G L K T D V T B Y H I D Q V S N L V E C L S D E F C  
76 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R  
77 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V  
78 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q  
79 L R G Y I E D S / Q D L E I Y L I R Y N A K H E T V N V P G T  
80 G S L W P L S A Q S P I G K C G E F N R C A P H L E W N P D  
81 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N  
82 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P  
83 L V G E A L K A R V K R A E K K W R D K R E K L E W E T N I V  
84 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H  
85 A A D K R V H S I R E A Y L P E L S V I F G V N A A I F E E  
86 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W  
87 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E  
88 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I  
89 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V  
90 N Q E E Y G G A Y T S R N R G Y N E A F S V P A D Y A S V Y  
91 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y  
92 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V  
93 E L L L M E E .

1           22. A pesticidal composition, according to claim  
2    12, wherein said gene, denoted pEW4, encoding a  
3    chimeric toxin, is as follows:

4	(start HD-1)	ATGG	ATAACAATCC	GAACATCAAT		
5	GAATGCATTC	CTTATAATTG	TTTAAGTAAC	CCTGAAGTAG	AAAGTATTAGG	600
6	TGGAGAAAGA	ATAGAAAATG	GTACACCCCC	AATCGATATT	TCCTTGTGCG	
7	TAACCGAATT	TCTTTGAGT	GAATTGTT	CCGGTGCTGG	ATTGTGTTA	700
8	GGACTAGTTG	ATATAATATG	GGGAATTTTT	GGTCCTCTC	AATGGGACGC	
9	ATTCCTGTG	CAAATTGAAC	AGTTAATTAA	CCAAAGAATA	GAAGAATTG	800
10	CTAGGAACCA	AGCCATTCT	AGATTAGAAG	GACTAAGCAA	TCTTTATCAA	
11	ATTACGCGAG	AATCTTTAG	AGAGTGGGAA	GCAGATCCTA	CTAATCCAGC	900
12	ATTAAGAGAA	GAGATGCGTA	TTCATTCAA	TGACATGAAC	AGTGCCTTA	
13	CAACCGCTAT	TCCTCTTTG	GCAGTTCAAA	ATTATCAAGT	TCCTCTTTA	1000
14	TCAGTATATG	TTCAAGCTGC	AAATTACAT	TTATCAGTTT	TGAGAGATGT	
15	TTCAGTGTGTT	GGACAAAGGT	GGGGATTG	TGCCGCGACT	ATCAATAGTC	1100
16	GTTATAATGA	TTTAACCTAGG	CTTATTGGCA	ACTATACAGA	TTATGCTGTG	
17	CGCTGGTACA	ATACGGGATT	AGAGCGTGT	TGGGGACCGG	ATTCTAGAGA	1200
18	TTGGGTAAGG	TATAATCAA	TTAGAAGAGA	GCTAACACTT	ACTGTATTAG	
19	ATATCGTTGC	TCTATTCTCA	AATTATGATA	GTCGAAGGTA	TCCAATTCGA	1300
20	ACAGTTCC	ATTAAACAAG	AGAAATTAT	ACGAACCCAG	TATTAGAAAA	
21	TTTGATGGT	AGTTTCGTG	GAATGGCTCA	GAGAATAGAA	CAGAATATTA	1400
22	GGCAACCACA	TCTTATGGAT	ATCCTTAATA	GTATAACCAT	TTATACTGAT	
23	GTGCATAGAG	GCTTTAATT	TTGGTCAGGG	CATCAAATAA	CAGCTTCTCC	1500
24	TGTAGGGTTT	TCAGGACCAG	AATTGCGATT	CCCTTATTT	GGGAATGCGG	
25	GGAATGCAGC	TCCACCCGTA	CTTGTCTCAT	TAACTGGTTT	GGGGATTTTT	1600
26	AGAACATTAT	CTTCACCTTT	ATATAGAAGA	ATTATACTTG	GTTCAGGGCCC	
27	AAATAATCAG	GAACGTGTTG	TCCTTGATGG	AACGGAGTTT	TCTTTTGCC	1700
28	CCCTAACGAC	CAACTTGCT	TCCACTATAT	ATAGACAAAG	GGGTACAGTC	
29	GATTCACTAG	ATGTAATACC	GCCACAGGAT	AATAGTGTAC	CACCTCGTGC	1800
30	GGGATTTAGC	CATCGATTGA	GTCATGTTAC	AATGCTGAGC	CAAGCAGCTG	
31	GAGCAGTTA	CACCTTGAGA	GCTCAACGT	(stop HD-1)		
32	(start HD-73)		CCT	ATGTTCTCTT		
33	GGATACATCG	TAGTGCTGAA	TTTAATAATA	TAATTGCATC	GGATAGTATT	1800
34	ACTCAAATCC	CTGCAGTGAA	GGGAAACTTT	CTTTTTAATG	GTTCGTAA	
35	TTCAGGACCA	GGATTACTG	GTGGGGACTT	AGTTAGATT	AATAGTAGTG	1900
36	GAAATAACAT	TCAGAATAGA	GGGTATATTG	AAGTTCCAAT	TCACTTCCCA	
37	TCGACATCTA	CCAGATATCG	AGTTCGTGT	CGGTATGCTT	CTGTAACCCC	2000
38	GATTCACCTC	AACGTTAATT	GGGGTAATT	ATCCATT	TCCAATACAG	
39	TACCAAGCTAC	AGCTACGTCA	TTAGATAATC	TACAATCAAG	TGATTTGGT	2100
40	TATTTGAAA	GTGCCAATGC	TTTACATCT	TCATTAGGTA	ATATAGTAGG	
41	TGTTAGAAAT	TTAGTGGGA	CTGCAGGAGT	GATAATAGAC	AGATTTGAAT	2200
42	TTATTCCAGT	TACTGCAACA	CTCGAGGCTG	AATATAATCT	GGAAAGAGCG	

30 CAGAAGGCAGG TGAATGCGCT GTTACGTCT ACAAAACCAAC TAGGGCTAAA 2300  
 31 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT  
 32 ATTTATCGGA TGAATTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400  
 33 GTCAAACATG CGAAGCGACT CAGTGATGAA CGCAATTAC TCCAAGATTG  
 34 AAATTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCGGAAGTA 2500  
 35 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTAAAGA AAATTACGTC  
 36 ACACTATCAG GTACCTTGA TGAGTGTAT CCAACATATT TGTATCAAAA 2600  
 37 AATCGATGAA TCAAAATTAA AAGCCTTTAC CCGTTATCAA TTAGAGGGT  
 38 ATATCGAAGA TAGTCAGAC TTAGAAATCT ATTTAATTG TGACAAATGCA 2700  
 39 AAACATGAAA CAGTAATGT GCCAGGTACG GGTTCTTAT GGCGCTTTC  
 40 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCGCGCCAC 2800  
 41 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAG  
 42 TGTGCCCATC ATTCGCATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900  
 43 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTAAG ATTAAGACGC  
 44 AAGATGGGCA CGCAAGACTA GGGAACTCTAG AGTTCTCGA AGAGAAACCA 3000  
 45 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAATGGAG  
 46 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAGAGG 3100  
 47 CAAAAGAATC TGTAGATGCT TTATTTGTAATC ACTCTCAATA TGATCAATTA  
 48 CAAGCGGATA CGAATATTGC CATGATTGAT GCGGCAGATA AACGTGTTCA 3200  
 49 TAGCATTGCA GAAGCTTATC TGCTGTAGCT GTCTGTGATT CGGGGTGTCA  
 50 ATGCGGCTAT TTTTGAAGAA TTAGAAGGSC GTATTTCAC TGCAATTCTCC 3300  
 51 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTTA ATAATGGCTT  
 52 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA ZAAAACAACC 3400  
 53 AACGTTCGGT CTTGTTGTT CCCGAATGGG AAGCAGAAAGT GTCACAAGAA  
 54 GTTCGTGTCT GTCCGGGTG TGCTGTATATC CTTCTGTCA CAGCGTACAA 3500  
 55 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAAATA  
 56 CAGACGAACT GAAGTTTAGC AATGCGTAG AAGAGGAAAT CTATCCAAAT 3600  
 57 AACACGGTAA CGTGTAAATGA TTAACTGTAA AATCAAGAAG AATAACGGAGG  
 58 TGCGTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAAG 3700  
 59 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAAGA  
 60 GAGAATCCTT GTGAATTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800  
 61 AGTTGGTTAT GTGACAAAAG AATTAGAATA CTTCCCAGAA ACCGATAAGG  
 62 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTATCGT GGACAGCGTG 3900  
 63 GAATTACTCC TTATGGAGGA A (end HD-73)

52 and equivalent nucleotide sequences coding for toxin  
 53 EW4 with the following amino acid sequence:

54 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E  
 55 T G Y T F I D I S L S L T Q F L L S E F V P G A G F V L G L  
 56 V D I I W G I F G P S Q W D A F P V Q I E Q L I N Q R I E E  
 57 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
 58 P T N P A L R E E M R I Q F N D M N S A L T T A I P L L A V  
 59 Q N Y Q V F L L S V Y V Q A A N L H L S V L R D V S V F G Q  
 60 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
 61 Y N T G L E R V W G F D S R D W V R Y N Q F R R E L T L T V  
 L D I V A L F S N Y D S R R Y P I R T V S Q L T R E I Y T N  
 P V L E N F D G S F R G M A Q R I E Q N I R Q P H L M D I L  
 N S I T I Y T D V H R G F N Y W S G H Q I T A S P V G F S G  
 P E F A F P L F G N A G N A A F P V L V S L T G L G I F R T

62 L S S P L Y R R I I L G S G P N N Q E L F V L D G T E F S F  
63 A S L T T N L P S T I Y R Q R G T V D S L D V I P P Q D N S  
64 V P P R A G F S H R L S H V T M L S Q A A G A V Y T L R A Q  
65 R P M F S W I H R S A E F N N I I A S D S I T Q I P A V K G  
66 N F L F N G S V I S G P G F T G G D L V R L N S S G N N I Q  
67 N R G Y I E V P I H F P S T S T R Y R V R V R Y A S Y T P I  
68 H L N V N W G N S S I F S N T V P A T A T S L D N L Q S S D  
69 F G Y F E S A N A F T S S L G N I V G V R N F S G T A G V I  
70 I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F  
71 T S T N Q L G L K T N V T D Y H I D Q V S N L V T Y L S D E  
72 F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N  
73 F K D I N R Q P E R G W G G S T G I T I Q G G D D V F K E N  
74 Y V T L S G T F D E C Y P T Y L Y Q K I D E S K L K A F T R  
75 Y Q L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P  
76 G T G S L W P L S A Q S P I G K C G E F N R C A P H L E W N  
77 P D L D C S C R D G E K C A H H S H H F S L D I D V G C T D  
78 L N E D L G V W V I F K I K T Q D G H A R L G N L E F L E E  
79 K P L V G E A L A R V K R A E K K W R D K R E K L E W E T N  
80 I V Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M  
81 I H A A D K R V H S I R E A Y L P E L S V I P G V N A A I F  
82 E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S  
83 C W N V K G H V D V E E Q N N Q R S V L V V P E W E A E V S  
84 Q E V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H  
85 E I E N N T D E L K F S N C V E E I Y P N N T V T C N D Y  
86 T V N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S  
87 V Y E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V  
88 G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D  
89 S V E L L M E E .

1           23. A pesticidal composition, according to claim  
2        12, wherein said gene, denoted pACB-1, encoding a  
3        chimeric toxin, is as follows:

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4          (start HD-73)          ATG GATAACAATC 400
5          CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
6          GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTTACACCC CAATCGATAT 500
7          TTCTTGTGCT CTAACGCAAT TTCTTTGAG TGAATTGTT CCCGGTGTG
8          GATTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTC TGGTCCCTCT 600
9          CAATGGGACG CATTCTTGT ACAAAATTGAA CAGTTAATTA ACCAAAGAAT
10         AGAAGAATTG GCTAGGAACC AAGCCATTTC TAGATTAGAA GGACTAAGCA 700
11         ATCTTATCA ATTACGCA GAATCTTTA GAGAGTGGGA AGCAGATCCT
12         ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
13         CAGTGCCCTT ACAACCGCTA TTCCCTTTT TGCAGTTCAA AATTATCAAG
14         TTCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
15         TTGAGAGATG TTTCAAGTGT TGGACAAAGG TGGGGATTG ATGCCGCGAC

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16 TATCAATACT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATAACAG 1000  
 17 ATTATGCTGT ACGCTGGTAC AATAACGGGAT TAGAACGTGT ATGGGGACCG  
 18 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100  
 19 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTACAAGAT  
 20 ATCCAATTG AACAGTTTCC CAATTAACAA GAGAAATTAA TACAAACCCA 1200  
 21 STATTAGAAA ATTTGATGG TAGTTTCGA GGCTCGGCTC AGGGCATAGA  
 22 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300  
 23 TCTATAACGGA TGCTCATAGG GGTTTATTATT ATTGGTCAGG GCATCAAATA  
 24 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400  
 25 TGGAACTATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG  
 26 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500  
 27 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT  
 28 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAAGCG 1600  
 29 GAACGGTAGA TTGCTGAAAT GAAATACCGC CACAGAATAA CAACGTGCCA  
 30 CCTAGGCAAG AATTAGTCA TCGATTAAGC CATGTTCAA TGTTTGTTC 1700  
 31 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)  
 32 (start HD-1) CCAACGT TTTCTGGCA GCATCGCAGT 1900  
 33 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT  
 34 AACAAAATCT ACTAATCTG GCTCTGGAAC TTGTGTCGTT AAAGGGACAG 2000  
 35 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTCA  
 36 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100  
 37 AATTGCGTAC GCTTCTACTA CAAATTACAA ATTCCATACA TCAATTGACG  
 38 GAAGACCTAT TAATCAGGGT AATTTCAG CAACTATGAG TAGTGGGAGT 2200  
 39 AATTTACAGT CCGGAAGCCTT TAGGACTATA GGTTTTACTA CTCCGTTAA  
 40 CTTTCAAAT GGATCAAGTG TATTAACTT AAGTGCTCAT GTCCTCAATT 2300  
 41 CAGGCAATGA AGTTTATATA GATCGAAATTG AATTGTTCC BGCAGAAAGTA  
 42 ACCTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400  
 43 GCTGTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT  
 44 ATCATATTGA TCAAGTATCC AATTAGTTG AGTGTTCATC AGATGAATT 2500  
 45 TGTCTGGATG AAAAACAAAGA ATTGTCGGAG AAAGTCAAAC ATGCGAAGCG  
 46 ACTTAACTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600  
 47 ATAGACAACG AGACCGGTGCG TGGAGAGGAA GTACGGATAT TACCATCCAA  
 48 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700  
 49 TGATGAGTGC TATCCAACGT ATTATATATCA AAAAATAGAT GAGTCGAAAT  
 50 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800  
 51 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA  
 52 TGTGCCAGGT ACGGGTTCTC TATGGCCGCT TTCAGCCCAA AGTCAAATCG 2900  
 53 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT  
 54 GACTTAGATT TTGCTGTAG GGATGGAGAA AAGTGTGCC ATCATTGCGA 3000  
 55 TCATTTCTCC TTAGACATTG ATGTAGGGATG TACAGACTTA AATGAGGACC  
 56 TAGGTGTATG GGTGATCTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
 57 CTAGGAAATC TAGAGTTCTC CGAAGAGAAA CCATTAGTAG GAGAAGCGCT  
 58 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTAAAAAAT 3200  
 59 TGGAAATGGGA AACAAATATC GTTATAAAAG AGGCAAAAGA ATCTGTAGAT  
 60 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAAGCGG ATACGAATAT 3300  
 61 TGCGATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCCTT  
 62 ATGTGCGCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTTGAA 3400  
 63 GAATTAGAAG GGCCTATTTC CACTGCATTC TCCCTATATG ATGCGAGAAA  
 64 TGTCAATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500  
 65 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCCCTGTT

66 CTTCCGGAAT GGGAAAGCAGA AGTGTACACAA GAAGTTCGTG TCTGTCCGGG 3600  
 67 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGAA TATGGAGAAAG  
 68 GTTGCCTAAC CATTGAGATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700  
 69 ABCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA  
 70 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
 71 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTATGCCTCAGTC  
 72 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAAATC CTTGTGAATT 3900  
 73 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
 74 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
 75 GAAACGGAAAG GAACATTAT CGTGGACAGC GTGGAATTAC TCCCTATGGA  
 76 GGAA (end HD-1)

77 and equivalent nucleotide sequences coding for toxin  
 78 ACB-1 with the following amino acid sequence:

79 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E  
 80 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L  
 81 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E  
 82 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
 83 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V  
 84 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q  
 85 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
 86 Y N T G L E R V W G P D S R D W V R Y N Q F R E L T L T V  
 87 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N  
 88 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L  
 89 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G  
 90 P E F T F P L Y G T M G N A A F Q Q R I V A Q L G Q G V Y R  
 91 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y  
 92 G T S S N L P S A V Y R K S G T V D S L N E I F P P Q N N N V  
 93 P P R Q E F S H R L S H V S M F R S G F S N S S V S I I R A  
 94 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T  
 95 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T  
 96 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S  
 97 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G  
 98 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D  
 99 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S  
 100 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C  
 101 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R  
 102 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V  
 103 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q  
 104 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T  
 105 G S L W P L S A Q S P I G K C G E F N R C A P H L E W N P D  
 106 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N  
 107 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P  
 108 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V  
 109 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H  
 110 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E

111 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S O W  
 112 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E  
 113 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I  
 114 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V  
 115 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y  
 116 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y  
 117 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V  
 118 E L L M E E .

1 24. A pesticidal composition, according to  
 2 claim 12, wherein said gene, denoted pSYW1, encoding  
 3 a chimeric toxin, is as follows:

4 (start HD-73) ATG GATAACAATC 400  
 5 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA  
 6 GAAGTATTAG GTGGAGAAAAG AATAGAAAATC GTTACACCC CAATCGATAT 500  
 7 TTCCCTTGTCG CTAACGCAAT TTCTTTGAG TGAATTGTT CCCGGTGCTG  
 8 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600  
 9 CAATGGGACG CATTCTTGT ACAAAATTGAA CAGTTAAATTA ACCAAAGAAT  
 10 AGAAGAATTG GCTAGGAACC AAGCCATTTC TAGATTAGAA GGACTAAGCA 700  
 11 ATCTTTATCA AATTACGCA GAATCTTTA GAGAGTGGGA AGCAGATCCT  
 12 ACTAAATCCAG CATTAAGAGA AGAGATCGT ATTCAATTCA ATGACATGAA 800  
 13 CAGTGCCCTT ACAACCCTA TTCCCTTTT TGCAAGTCAA AATTATCAAG  
 14 TTCCCTTTT ATCACTATAT GTTAAAGCTG CAAATTACA TTTATCAGTT 900  
 15 TTGAGAGATG TTTCAGTGGT TGGACAAAGG TGGGGATTTG ATGCCGCGAC  
 16 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000  
 17 ATTATGCTGT ACGCTGGTAC AATAACGGGAT TAGAACGTTG ATGGGGACCG  
 18 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAAGAG AATTAACACT 1100  
 19 AACTGTATTA GATATCGTGT CTCTGTTCCC GAATTATGAT AGTAGAAGAT  
 20 ATCCAATTG AACAGTTTCC CAATTAACAA GAGAAATTAA TACAAACCCA 1200  
 21 GTATTAGAAA ATTGATGG TAGTTTCGA GGCTCGGCTC AGGGCATAGA  
 22 AGGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300  
 23 TCTATACGGA TGCTCATAAA GGGGAATATT ATTGGTCAGG GCATCAAATA  
 24 ATGGCTCTC CTCTAGGTT TTCCGGGSCCA GAATTCACTT TTCCGCTATA 1400  
 25 TGGAACTATG GGAAATGCGAG CTCCACAAACA ACGTATTGTT GCTCAACTAG  
 26 GTCAGGGCGT GTATAGAACCA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500  
 27 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT  
 28 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAAGCG 1600  
 29 GAACGGTAGA TTGCGTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA  
 30 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTCAA TGTTCGTTC 1700  
 31 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)  
 32 (start HD-1) CCAACGT TTTCTGGCA GCATCGCAGT 1900  
 33 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT  
 34 AACAAAATCT ACTAATCTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAAG 2000  
 35 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTTC  
 36 ACCTTAAGAG TAAATATTAC TGCAACCATTA TCACAAAGAT ATCGGGTAAG 2100  
 37 AATTGCGTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG  
 38 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200  
 39 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTAA  
 40 CTTTCAAAT GGATCAAGTG TATTACGTT AAGTGCTCAT GTCTTCAATT 2300  
 41 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAAGTA

42 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400  
43 GCTGTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT  
44 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATT 2500  
45 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG  
46 ACTTAGTGT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600  
47 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA  
48 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700  
49 TGATGAGTGC TATCCAACGT ATTATATCA AAAAATAGAT GAGTCGAAAT  
50 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800  
51 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA  
52 TGTGCCAGGT ACGGGTTCCCT TATGGCCGCT TTCAGCCAA ATCCAATCG 2900  
53 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT  
54 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCCG ATCATTGCGA 3000  
55 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC  
56 TAGGTGTATG GGTGATCTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
57 CTAGGGAATC TAGAGTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT  
58 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTGAAGAAAT 3200  
59 TGGAATGGGA AACAAATATC GTTTATAAAG AGGGAAGAAAGA ATCTGTAGAT  
60 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300  
61 TGCCATGATT CATGCGCGAG ATAAACGTGT TCAATAGCATT CGAGAAGCGTT  
62 ATCTGCCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400  
63 GAATTAGAAG GGCCTATTTT CACTGCTTC TCCCTATATG ATGCGAGAAA  
64 TGTCATTAAA AATGGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500  
65 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTG GGTCTTGTGTT  
66 CTTCCGGAAT GGGAAAGCAGA AGTGTCAAAA GAAGTTCGTG TCTGTCCGGG 3600  
67 TCGTGGCTAT ATCCTTCGTG TCAACASCGTA CAAGGGAGGGA TATGGAGAAG  
68 GTTGCCTAAC CATTGATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700  
69 AGCAACTGCG TAGAAGAGGA AATCTATCAGA AATAACACGG TAACGTGTAA  
70 TGATTATACT GTAAATCAAG AAGAATAACGG AGGTGCGTAC ACTTCTCGTA 3800  
71 ATCGAGGATA TAACGAAGCT ECTTCCGTAC CAGCTGATTA TGCCTCAGTC  
72 TATGAAGAAA AATCGTATAC AGATGACGA AGAGAGAAC TCTGTGAATT 3900  
73 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
74 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
75 GAAACGGAAG GAACATTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA  
76 GGAA (end HD-1)

77 and equivalent nucleotide sequences coding for toxin  
78 SYW1 with the following amino acid sequence:

79 M D N N P N I N E C I F Y N C L S N P E V E V L G G E R I E  
80 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L  
81 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E  
82 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
83 P T N P A L R E E M R I Q F N D M N S A L T T A I F L F A V  
84 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q  
85 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
86 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V  
87 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N  
88 P V L E N F D G S F R G G S A Q G I E G S I R S P H L M D I L  
89 N S I T I Y T D A H K G E Y Y W S G H Q I M A S P V G F S G  
90 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R

91 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y  
 92 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V  
 93 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A  
 94 P T F S W Q H R S A E F N N I I P P S S Q I T Q I P L T K S T  
 95 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T  
 96 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S  
 97 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G  
 98 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D  
 99 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S  
 100 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C  
 101 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R  
 102 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V  
 103 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q  
 104 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T  
 105 G S L W P L S A Q S P I G K C G E F N R C A P H L E W N P D  
 106 L D C S C R D G E K C A H H S H H F S D I D V G C T D L N  
 107 E D L G Y W V I F K I K T Q D G H A R L G N L E F L E E K P V  
 108 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I  
 109 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H  
 110 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E  
 111 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W  
 112 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E  
 113 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I  
 114 E N N T D E L K F S N C V E E I Y P N N T V T C N D Y T V  
 115 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y  
 116 E E K S Y T D G R G R E N P C E F N R G Y R D Y T P L P V G Y  
 117 V T K E L E Y F P E T D K V V W I E I G E T E G T F I V D S V  
 118 E L L L M E E

1 25. A recombinant DNA transfer vector comprising  
 2 DNA having the following nucleotide sequence or  
 3 equivalent nucleotide sequences containing bases whose  
 4 translated region codes for the same amino acid sequence:

5 (start HD-73) ATG GATAACAATC 400  
 6 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA  
 7 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTTACACCC CAATCGATAT 500  
 8 TTCCCTTGTCG CTAACGCAAT TTCTTTGAG TGAATTGTT CCCGGTGCTG  
 9 GATTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600  
 10 CAATGGGACG CATTCTTGT ACAAAATTGAA CAGTTAATTAA ACCAAAGAAT  
 11 AGAAGAATTG GCTAGGAACC AAGCCATTTC TAGATTAGAA GGACTAAGCA 700  
 12 ATCTTATCA AATTACGCA GAATCTTTA GAGAGTGGGA AGCAGATCCT  
 13 ACTAATCCAG CATTAAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800  
 14 CAGTGCCTT ACAACCGCTA TTCTCTTT TGCAAGTCAA AATTATCAAG  
 15 TTCCCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900  
 16 TTGAGAGATG TTTCAGTGT TGACAAAGG TGGGGATTTG ATGCCGCGAC  
 17 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000  
 18 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG  
 19 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100  
 20 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT  
 21 ATCCAATTG AACAGTTTCC CAATTAACAA GAGAAATTAA TACAAACCCA 1200  
 22 GTATTAGAAA ATTTTGATGG TAGTTTCCGA GGCTCGGCTC AGGGCATAGA

23 AAGAAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300  
24 TCTATACGGA TGCTCATAGG GGTTATTATT ATTGGTCAGG GCATCAAATA  
25 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400  
26 TGGAACTATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG  
27 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTT 1500  
28 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT  
29 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAAC AGAAAAAGCG 1600  
30 GAACGGTAGA TTGCTGGAT GAAATACCGC CACAGAAATAA CAACGTGCCA  
31 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTCAA TGTTTGTTC 1700  
32 AGGCTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end HD-73)  
33 (start HD-1) CCAACGT TTTCTGGCA GCATCGCAGT 1900  
34 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTT  
35 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTGCGTT AAAGGACCAAG 2000  
36 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTCA  
37 ACCTTAAGAG TAAATATTAC TGCACTTAA TCACAAABAT ATCGGGTAAG 2100  
38 AATTGCGTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG  
39 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200  
40 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTAA  
41 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGTCTAT GTCTTCAATT 2300  
42 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA  
43 ACCTTGAGG CAGAATATGA TTTAGAAAAGA GCACAAAAGG CGGTGAATGA 2400  
44 GCTGTTTACT TCTTCCAATC AAACTGGGTT AAAAACAGAT GTGACGGATT  
45 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTTATC AGATGAATT 2500  
46 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG  
47 ACTTAGTGAT GAGCGGAATT TACCTCAAGA CCAAACTTC AGAGGGATCA 2600  
48 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA  
49 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700  
50 TGATGAGTGC TATCCAACGT ATTATATCA AAAAATAGAT GAGTCGAAAT  
51 TAAAAGCTA TACCGTTAT CAATTAAAGAG GGTATATCGA AGATAGTCAA 2800  
52 GACTTAGAAA TCTATTTAAT TCGTACAAT GCAAAACATG AAACAGTAAA  
53 TGTGCCAGGT ACGGGTTCTT TATGCCGCT TTCAGCCCAA AGTCCAATCG 2900  
54 GAAAGTGTGG AGAGCCGAAT CGATGCGCAG CACACCTTGA ATGGAATCCT  
55 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000  
56 TCATTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC  
57 TAGGTGTATG GGTGATCTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
58 CTAGGGAATC TAGAGTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT  
59 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTAAAAAAT 3200  
60 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT  
61 GCTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300  
62 TGCCATGATT CATGCGGAG ATAAACGTGT TCATAGCATT CGAGAAGCTT  
63 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400  
64 GAATTAGAAG GCGTATTCTT CACTGCATTC TCCCTATATG ATGCGAGAAA  
65 TGTCATTAAG AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500  
66 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCTTGTGTT  
67 CTTCCGGAAT GGGAAAGCAGA AGTGTACCAA GAAGTTCGTG TCTGTCCGGG 3600  
68 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG  
69 GTTGCCTAAC CATTGATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700  
70 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA  
71 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
72 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCGTCAGTC  
73 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900  
74 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
75 AAGAATTAGA ATACTTCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
76 GAAACGGAAG GAACATTAT CGTGGACAGC GTGGAAATTAC TCCTTATGGGA  
77 GGAA (end HD-1).

1           26. A recombinant DNA transfer vector comprising  
2        DNA having the following nucleotide sequence or ,  
3        equivalent nucleotide sequences containing bases whose  
4        translated region codes for the same amino acid sequence:

5 (start HD-1) ATGG ATAACAATCC GAACATCAAT  
 6 GAATGCATTC CTTATAATTG TTTAAGTAA CCTGAAGTAG AAGTATTAGG 600  
 7 TGGAGAAAGA ATAGAAACTG GTTACACCCC AATCGATATT TCCTTGTCGC  
 8 TAACGCAATT TCTTTGAGT GAATTTGTT CCGGTGCTGG ATTTGTGTTA 700  
 9 GGACTAGTTG ATATAATATG GGGAAATTTT GGTCCCTCTC AATGGGACGC  
 10 ATTTCTGTG CAAATTGAAC AGTTAATTAA CAAAGAATA GAAGAATTG 800  
 11 CTAGGAACCA AGCCATTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA  
 12 ATTTACGCGAG AATCTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900  
 13 ATTAAGAGAA GAGATGCGTA TTCATTCAA TGACATGAAC AGTGCCTTA  
 14 CAACCGCTAT TCCCTTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTA 1000  
 15 TCAGTATATG TTCAAGCTGC AAATTACAT TTATZAGTT TGAGAGATGT  
 16 TTCAAGCTGC 1100  
 17 GTTATAATGA TTTAACTAGG CTTATTGGCA ACTATACAGA TTATGCTGTG  
 18 CGCTGGTACA ATACGGGATT AGAGCCTGTA TGGGGACCGG ATTCTAGAGA 1200  
 19 TTGGGTAAGG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG  
 20 ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTGCA 1300  
 21 ACAGTTTCCC AATTAAACAAG AGAAAATTAT ACGAACCCAG TATTAGAAAA  
 22 TTTGATGGT AGTTTCGTG GAATGGCTCA GAGAATABAA CAGAATATTA 1400  
 23 GGCACCCACA TCTTATGGAT ATCCCTAATA GTATAACCAT TTATACTGAT  
 24 GTGCATAGAG GCTTTAATT TTGGTCAGGG CATCAAATAA CAGCTTCTCC 1500  
 25 TGTAGGGTTT TCAGGACCAAG AATTTCGATT CCCTTTATTG GGGAATGCGG  
 26 GGAATGCAGC TCCACCCGTA TTGTCCTCAT TAACTGGTTT GGGGATTTTT 1600  
 27 AGAACATTAT CTTCACCTTT ATATAGAAGA ATTATACTTG GTTCAGGCC  
 28 AAATAATCAG GAACTGTTTG TCCATTGATGG AACGGAGTTT TCTTTGCTC 1700  
 29 CCCTAACGAC CAACTTGCT TCACTATAT ATAGACAAAG GGGTACAGTC  
 30 GATTCACTAG ATGTAATACC GCCACAGGAT AATAGTGTAC CACCTCGTGC 1800  
 31 GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG  
 32 GAGCAGTTA CACCTTGAGA GCTCAACGT (stop HD-1)  
 33 (start HD-73) CCT ATGTTCTCTT  
 34 GGATACATCG TAGTGCTGAA TTTAATAATA TAATTGCATC GGATAGTATT 1800  
 35 ACTCAAATCC CTGCAGTGAA GGGAAACTTT CTTTTAATG GTTCTGTAAT  
 36 TTCAGGACCA GGATTTACTG GTGGGGACTT AGTTAGATTA AATAGTAGTG 1900  
 37 GAAATAACAT TCAGAATAGA GGGTATATTG AAGTCCAAT TCACTTCCA  
 38 TCGACATCTA CCAGATATCG AGTTCGTGTG CGGTATGCTT CTGTAACCCC 2000  
 39 GATTACCTC AACGTTAATT GGGGTAAATT ATCCATTTC TCCAATACAG  
 40 TACCAAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTGGT 2100  
 41 TATTTGAAA GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG  
 42 TGTTAGAAAT TTTAGTGGGA CTGCAGGGAGT GATAATAGAC AGATTTGAAT 2200  
 43 TTATTCCAGT TACTGCAACA CTCGAGGGCTG AATATAATCT GGAAAGAGCG  
 44 CAGAAGGCGG TGAATGCCT GTTACGTCT ACAAAACCAAC TAGGGCTAAA 2300  
 45 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT  
 46 ATTTATCGGA TGAATTTCGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400  
 47 GTCAAACATG CGAAGCGACT CAGTGTGAA CGCAATTAC TCCAAGATTC  
 48 AAATTTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCGGAAGTA 2500  
 49 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAAGA AAATTACGTC  
 50 ACACATATCAG GTACCTTGAA TGAGTGTCTAT CCAACATATT TGTATCAAA 2600  
 51 AATCGATGAA TCAAAATTAA AAGCCTTAC CCGTTATCAA TTAAGAGGGT

52 ATATCGAAGA TAGTCAAGAC TTAGAAAATCT ATTTAATTG CTACAATGCA 2700  
 53 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCCTAT GGCGCGTTTC  
 54 AGCCCCAAAGT CCAATCGGAA AGTGTGAGA GCCGAATCGA TGCGCGCCAC 2800  
 55 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGG TGGAGAAAAG  
 56 TGTGCCCATC ATTGCGATCA TTTCTCCCTA GACATTGATG TAGGATGTAC 2900  
 57 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC  
 57 AAGATGGGCA CGCAAGACTA GGGAACTAG AGTTTCTCGA AGAGAAAACCA 3000  
 59 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAATGGAG  
 60 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAAGAGG 3100  
 61 CAAAAGAACATC TGAGATGCT TTATTTGAA ACTCTCAATA TGATCAATT  
 62 CAAGCGGATA CGAATATTGC CATGATTATCAT GCGGCAGATA AACGTGTTCA 3200  
 63 TAGCATTGCA GAAGCTTATC TGCTGTGAGCT GTCTGTGATT CCGGGTGTCA  
 64 ATGCGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTCACT TGCATTCTCC 3300  
 65 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTTTA ATAATGGCTT  
 66 ATCCTGCTGG AACGTGAAAG GGCAATGAGA TGTAGAAGAA CAAAACAACC 3400  
 67 AACGTTCGGT CCTTGTGTT CCGGAATGGG AAGCAGAAGT GTCACAAGAA  
 68 GTTCGTGTCT GTCCGGGTCTG TGGCTATATC CTTGTGTCA CAGCGTACAA 3500  
 69 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAAATA  
 70 CAGACGAACG GAAAGTTTAGC AACTGCGTAG AAGAGGAAAT CTATCCAAT 3600  
 71 AACACGGTAA CGTGTAAATGA TTATACGTAA AATCAAGAAG AATAACGGAGG  
 72 TGCGTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAAG 3700  
 73 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATAACAGA TGGACGAAGA  
 74 GAGAATCCCT GTGAATTAA CAGAGGGTAT AGGGATTACAA CGCCACTACC 3800  
 75 AGTTGGTTAT GTGACAAAAG AATAGAATA CTTCCCAGAA ACCGATAAGG  
 76 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTATCGT GGACAGCGTG 3900  
 77 GAATTACTCC TTATGGAGGA A (end HD-73).

1 27. A recombinant DNA transfer vector comprising  
 2 DNA having the following nucleotide sequence or  
 3 equivalent nucleotide sequences containing bases whose  
 4 translated region codes for the same amino acid  
 5 sequence:

6 (start HD-73) ATG GATAACAATC 400  
 7 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA  
 8 GAAGTATTAG GTGGAGAAAAG AATAGAAAAT GGTTACACCC CAATCGATAT 500  
 9 TTCTTGTCG CTAACGCAAT TTCTTTGAG TGAATTGTT CCCGGTGCTG  
 10 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTAA TGGTCCCTCT 600  
 11 CAATGGGACG CATTCTTGT ACAAAATTGAA CAGTTAATTA ACCAAAGAAAT  
 12 AGAAGAAATTC GCTAGGAACC AAGCCATTTC TAGATTAGAA GGACTAAGCA 700  
 13 ATCTTTATCA AATTTCAGCA GAATCTTTA GAGAGTGGGA AGCAGATCCT  
 14 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800  
 15 CAGTGCCTT ACAACCGCTA TTCCCTTTT TGCAAGTTCAA AATTATCAAG  
 16 TTCCCTTTT ATCAAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900  
 17 TTGAGAGATG TTTCAGTGTGTT TGGACAAAGG TGGGGATTTG ATGCCGCGAC  
 18 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000  
 19 ATTATGCTGT ACGCTGGTAC AATAACGGGAT TAGAACGTGT ATGGGGACCG  
 20 GATTCTAGAG ATGGGTAAG GTATAATCAA TTAGAGAAGAG AATTAACACT 1100  
 21 AACTGTATTA GATATCGTTG CTCTGTCCCC GAATTATGAT AGTAGAAGAT

22 ATCCAATTCTG AACAGTTCC CAATTAACAA GAGAAATTAA TACAAACCCA 1200  
 23 GTATTAGAAA ATTTGATGG TAGTTTCSA GGCTCGGCTC AGGGCATAGA  
 24 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300  
 25 TCTATACGGA TGCTCATAGG GGTATTATTATT ATTGGTCAGG GCATCAAATA  
 26 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400  
 27 TGGAACTATG GGAAATGCAG CTCACAAACA ACGTATTGTT GCTCAACTAG  
 28 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTT 1500  
 29 AATATAGGGAA TAAATAATCA ACAACTATCT GTTCTGACG GGACAGAATT  
 30 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600  
 31 GAACGGTAGA TTCGCTGAAT GAAATACCGC CACAGAATAA CAACGTGCCA  
 32 CCTAGGCAAG AATTTAGTCA TCGATTAAGC CATGTTCAA TGTTCGTTC 1700  
 33 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)  
 34 (start HD-1) CCAACGTTTCTTGBCA GCATCGCAGT 1900  
 35 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT  
 36 AACAAAATCT ACTAATCTTGT GCTCTGGAAC TTCTGTCGTT AAAGGACCG 2000  
 37 GATTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTCA  
 38 ACCTTAAGAG TAAATATTAC TGACCATTA TGACAAAGAT ATCGGGTAAG 2100  
 39 AATTGCGTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG  
 40 GAAGACCTAT TAATCAGGGT AATTTTTCAAG CAACTATGAG TAGTGGGAGT 2200  
 41 AATTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTAA  
 42 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCATT 2300  
 43 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA  
 44 ACCTTGAGG CAGAATATGA TTAGAGAAAGA GCACAAAAAGG CGGTGAATGA 2400  
 45 GCTGTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT  
 46 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTGTTATC AGATGAATT 2500  
 47 TGTCTGGATG AAAAACAGA ATTGTCCGAG AAAGTCAAAC ATSGAAGCG  
 48 ACTTAGTGTG GAGCGAAATT TACTTCAGA TCCAAACTTC AGAGGGATCA 2600  
 49 ATAGACAACG AGACCGTGGC TGGAGAGGGAA GTACGGATAT TACCATCAA  
 50 GGAGGCGATG ACGTATTCAGA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700  
 51 TGATGAGTGC TATCDAACGT ATTATATATCA AAAAATAGAT GAGTCGAAAT  
 52 TAAAAGCCTA TACCGTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800  
 53 GACTTAGAAA TGTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA  
 54 TGTGCCAGGT ACGGGTTCCCT TATGGCCGCT TTCAGCCCCA AGTCCAATCG 2900  
 55 GAAAATGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT  
 56 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCA 3000  
 57 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC  
 58 TAGGTGTATG GGTGATCTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
 59 CTAGGGAAATC TAGAGTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT  
 60 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTGAAAAAT 3200  
 61 TGGAAATGGGA AACAAATATC GTTATAAAG AGGCAAAAGA ATCTGTAGAT  
 62 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAAGCGG ATACGAATAT 3300  
 63 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT  
 64 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400  
 65 GAATTAGAAG GGCCTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA  
 66 TGTCATTAAA AATGGTGTATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500  
 67 AAGGSCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCCCTGTT  
 68 CTTCCGGAAT GGGAAAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600  
 69 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGAA TATGGAGAAG  
 70 GTTGCCTAAC CATTGATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700  
 71 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGAA

72 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
 73 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATT TGCGTCAGTC  
 74 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900  
 75 TAACAGAGGG TATAAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
 76 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
 77 GAAACGGAAAG GAACATTAT CGTGGACACGC GTGGAATTAC TCCTTATGGAA  
 78 GGAA (end HD-1).

1           28. A recombinant DNA transfer vector comprising  
2 DNA having the following nucleotide sequence or  
3 equivalent nucleotide sequences containing bases whose  
4 translated region codes for the same amino acid  
5 sequence:

		(start HD-73)			
6	CGAACATCAA	TGAATGCATT	CCTTATAATT	GTAAAGTAA	ATG GATAACAATC 400
7	GAAGTATTAG	GTGGAGAAAAG	AATAGAAAAC	GGTTACACCC	CCCTGAAAGTA 500
8	TTCCTGTGCG	CTAACGCAAT	TTCTTTGAG	TGAATTGT	CAATCGATAT CCCGGTGTG
9	GATTTGTGTT	AGGACTAGTT	GATATAATAT	GGGGAATT	TGGTCCCTCT 600
10	CAATGGGACG	CATTTCTTGT	ACAAATTGAA	CAGTTAATT	ACCAAAGAAT
11	AGAAGAATT	GCTAGGAACC	AGGCCATTTC	TAGATTAGAA	GGACTAAGCA 700
12	ATCTTATCA	AATTTACGCA	GAATCTT	GAGAGTGGGA	AGCAGATCCT
13	ACTAATCCAG	CATTAAGAGA	AGAGATGCGT	ATTCAATTCA	ATGACATGAA 800
14	CAGTGCCTT	ACAAACCGCTA	TTCTCTTTT	TGCAAGTTCAA	AATTATCAAG
15	TTCCCTTTT	ATCAGTATAT	GTTCAACTG	CAAATTACA	TTTATCAGTT 900
16	TTGAGAGATG	TTTCAGTGT	TGGACAAAAGG	TGGGATT	ATGCCGCGAC
17	TATCAATAGT	CGTTATAATG	ATTTAACTAG	GCTTATTGGC	AACTATACAG 1000
18	ATTATGCTGT	ACGCTGGTAC	AATACGGGAT	TAGAACGTGT	ATGGGGACCG
19	GATTCTAGAG	ATTGGSTAAG	GTATAATCAA	TTTAAAGAG	AATTAAACACT 1100
20	AACTGTATT	GATATCGTT	CTCTGTTCCC	GAATTATGAT	AGTABAAGAT
21	ATCCAATT	AACAGTTCC	CAATTAAACAA	GAGAAATT	TACAAACCCA 1200
22	GTATTAGAAA	ATTTTGATGG	TAGTTTCGA	GGCTCGGCTC	AGGGCATAGA
23	AGGAAGTATT	AGGAGTCAC	ATTGATGGA	TATACTTAAC	AGTATAACCA 1300
24	TCTATACGGA	TGCTCATAAA	GGGAATATT	ATTGGTCAGG	GCATCAAATA
25	ATGGCTTTC	CTGTAGGGTT	TTGGGGGCCA	GAATTCACTT	TTCCGCTATA 1400
26	TGGAACATG	GGAAATGCAG	CTCCACAAACA	ACGTATTGTT	GCTCAACTAG
27	GTCAGGGCGT	GTATAGAAC	TTATCGTCCA	CTTTATATAG	AAGACCTTT 1500
28	AATATAGGGA	TAATAATCA	ACAACATATCT	GTTCTGACG	GGACAGAATT
29	TGCTTATGGA	ACCTCCTCAA	ATTGCCATC	CGCTGTATAC	AGAAAAAGCG 1600
30	GAACGGTABA	TTCGCTGGAT	GAAATACCGC	CACAGAATAA	CAACGTGCCA
31	CCTAGGCAAG	GATTTAGTCA	TGCAATTAGC	CATGTTTCAA	TGTTTCGTT 1700
32	AGGCTTTAGT	AAATAGTAGTG	TAAGTATAAT	AAGAGCT	(end hd-73)
33	(start HD-1)		CCAACGT	TTTCTGGCA	GCATCGCACT 1900
34	GCTGAATT	ATAATATAAT	TCCTTCATCA	CAAATTACAC	AAATACCTT
35	AACAAAATCT	ACTAATCTTG	GCTCTGGAAC	TTCTGTCGTT	AAAGGACCG 2000
36	GATTTACAGG	AGGAGATATT	CTTCGAAGAA	CTTCACCTGG	CCAGATTCA
37	ACCTTAAGAG	TAATATTAC	TGCAACCATTA	TCACAAAGAT	ATCGGGTAAG 2100
38	AATTGCGTAC	GCTTCTACTA	CAAATTACA	ATTCCATACA	TCAATTGACG
39					

40 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200  
 41 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTAA  
 42 CTTTCAAT GGATCAAGTG TATTACGTT AAGTGCTCAT GTCTTCAATT 2300  
 43 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAAGTA  
 44 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400  
 45 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT  
 46 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATT 2500  
 47 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG  
 48 ACTTAGTGT GAGCGGAATT TACTTCAAGA TCCAAACTC AGAGGGATCA 2600  
 49 ATAGACAAC AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA  
 50 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGTACCTT 2700  
 51 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT BAGTCGAAAT  
 52 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCBA AGATAGTCAA 2800  
 53 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA  
 54 TGTGCCAGGT ACGGGTTCTT TATGGCCGCT TTCAGCCAA AGTCCAATCG 2900  
 55 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT  
 56 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCC ATCATTGCGA 3000  
 57 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC  
 58 TAGGTGTATG GGTGATCTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
 59 CTAGGGAAATC TAGAGTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT  
 60 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTGAAGAAAT 3200  
 61 TGGAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT  
 62 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300  
 63 TGCATGATT CATGCGGCGAG ATAAACGTGT TCATAGCATT CGAGAAGCTT  
 64 ATCTCGCTGA BCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400  
 65 GAATTAGAAG GGCATTTT CACTGCATTTC TCCCTATATG ATGCAGAGAAA  
 66 TGTATTAA AATGGTGATT TTAATAAATGG CTTATCCTGC TGGAACGTGA 3500  
 67 AAGGGCATGT AGATGTAGAA GAACAAACAA ACCAACCGTTC GGTCTTGT  
 68 CTTCCGGAAT GGGAAAGCAGA AGTGTACCAA GAAGTTCGTG TCTGTCCGGG 3600  
 69 TCSTGGCTAT ATCCTTCGTG TCAACAGCGTA CAAGGAGGGA TATGGAGAAG  
 70 GTTGCCTAAC CATTATGAG ATCGAGAAACA ATACAGACGA ACTGAAGTTT 3700  
 71 AGCAACTGCG TAGAAGAGGAA AATCTATCCA AATAACACGG TAACGTGTAA  
 72 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
 73 ATCGAGGATA TAACGAAGCT CCTTCGTCAC CAGCTGATTA TGCGTCAGTC  
 74 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAAATC CTTGTGAATT 3900  
 75 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
 76 AAGAATTAGA ATACCTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
 77 GAAACGGAAG GAACATTTAT CGTGGACACGC GTGGATTAC TCCTTATGGGA  
 78 GGAA (end HD-1).

1 29. The DNA transfer vector of claim 25 trans-  
 2 ferred to and replicated in a prokaryotic or lower  
 3 eukaryotic microorganism.

1       30. The DNA transfer vector of claim 26 transferred to and replicated in a prokaryotic or lower  
2       eukaryotic microorganism.

1       31. The DNA transfer vector of claim 27 transferred to and replicated in a prokaryotic or lower  
2       eukaryotic microorganism.

1       32. The DNA transfer vector of claim 28 transferred to and replicated in a prokaryotic or lower  
2       eukaryotic microorganism.

1       33. Plasmid pEW1 as shown in FIGURE 1 of the  
2       drawings.

1       34. Plasmid pEW2 as shown in FIGURE 2 of the  
2       drawings.

1       35. Plasmid pEW3 as shown in FIGURE 3 of the  
2       drawings.

1       36. Plasmid pEW4 as shown in FIGURE 4 of the  
2       drawings.

1       37. Plasmid pACB-1, having the construction of  
2       plasmid pEW3 except that the DNA encoding aspartic  
3       acid at position 411 is converted to encode asparagine,  
4       and the DNA encoding glycine at position 425 is con-  
5       verted to encode glutamic acid.

1       38. Plasmid pSYW1, having the construction of plasmid  
2       pEW3 except that the DNA encoding arginine at position  
3       289 is converted to encode glycine, the DNA encoding  
4       arginine at position 311 is converted to encode lysine,  
5       and the DNA encoding tyrosine at position 313 is conver-  
6       ted to encode glutamate.

1           39. A microorganism transformed by the transfer  
2       vector of claim 25.

1           40. A microorganism transformed by the transfer  
2       vector of claim 26.

1           41. A microorganism transformed by the transfer  
2       vector of claim 27.

1           42. A microorganism transformed by the transfer  
2       vector of claim 28.

1           43. E. coli (pEW3), a microorganism according  
2       to claim 39.

1           44. E. coli (pEW4), a microorganism according to  
2       claim 40.

1           45. E. coli (pACB-1), a microorganism according  
2       to claim 41.

1           46. E. coli (pSYW1), a microorganism according  
2       to claim 42.

1           47. A process for preparing pesticidal chimeric  
2       toxin EW3 having the following amino acid sequence:

3       M D N N P N I N E C I F Y N C L S N P E V E V L G G E R I E  
4       T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L  
5       V D I I W G I F G F S Q W D A F L V Q I E Q L I N Q R I E E  
6       F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
7       P T N F A L R E E M R I Q F N D M N S A L T T A I P L F A V  
8       Q N Y Q V F L L S V Y V Q A A N L H L S V L R D V S V F G Q  
9       R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
10       Y N T G L E R V W G F D S R D W V R Y N Q F R R E L T L T V  
11       L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N  
12       F V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L  
13       N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G

14 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R  
15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y  
16 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V  
17 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A  
18 P T F S W Q H R S A E F N N I I F S S Q I T Q I P L T K S T  
19 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T  
20 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S  
21 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G  
22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D  
23 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S  
24 S N Q I G L K T D V T D O Y H I D Q V S N L V E C L S D E F C  
25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R  
26 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V  
27 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q  
28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V F G T  
29 G S L W P L S A Q S P I G K C G E F N R C A P H L E W N P D  
30 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N  
31 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P  
32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V  
33 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H  
34 A A D K R V H S I R E A Y L F E L S V I P G V N A A I F E E  
35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W  
36 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E  
37 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I  
38 E N N T D E L K F S N Q V E E E I Y P N N T V T C N D Y T V  
39 N Q E E Y G G A Y T S R N R S Y N E A P S V P A D Y A S V Y  
40 E E K S Y T D G R R E N F C E F N R G Y R D Y T P L P V G Y  
41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V  
42 E L L L M E E

43 which comprises culturing a prokaryotic microbe  
44 hosting a recombinant DNA transfer vector, denoted  
45 pEW3, comprising DNA having the following nucleotide  
46 sequence or equivalent nucleotide sequences containing  
47 bases whose translated region codes for the same  
48 amino acid sequence:

49 (start HD-73) ATG GATAACAATC 400  
50 C G A A C A T C A A T G A A T G C A T T C C T T A T A A T T G T T A A G T A A C C C T G A A G G T A  
51 G A A S T A T T A G G T G G G A G A A A G A A T A G A A A C T G G T T A C A C C C C A A T C G A T A T 500  
52 T T C C T T G T C G C T A A C G C A A T T T C T T T G A G G T G A A T T T G T T C C C G G T G C T G  
53 G A T T T G T G T T A G G A C T A G T T G A T A T A T T G G G G A A T T T T T G G T C C C T C T 600  
54 C A A T G G G A C G C A T T T C T T G T A C A A A T T G A A C A G T T A A T T A C C C A A A G G A A T  
55 A G A A G A A T T C G C T A G G A A C C A G G C C A T T T C T A G A T T A G G A A G G A C T A A G C A 700  
56 A T C T T T A T C A A A T T T A C G C A G A A T C T T T T A G A G A T G G G A A G C A G A T C C T  
57 A C T A A T C C A G C A T T A A G A G A G A G A T G C G T A T T C A A T T C A A T G A C A T G A A 800  
58 C A G T G C C C T T A C A A C C G C T A T T C C T C T T T T G C A G T T C A A A T T T A C A A T T A T C A A G  
59 T T C C T C T T T T A T C A G T A T A T G T C A A G C T G C A A A T T T A C A A T T A T C A G T T 900  
60 T T G A G A G A T G T T T C A G T G T T T G G A C A A A G G T G G G G A T T T G A T G C C G C G A C

61 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATAACAG 1000  
62 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG  
63 GATTCTAGAG ATTGGGTAAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100  
64 AACTGTATTA GATATCGTTG CTCGTGTCCTC GAATTATGAT AGTAGAAGAT  
65 ATCCAATTG AACAGTTTC CAAATTAACAA GAGAAATTAA TACAAACCCA 1200  
66 GTATTAGAAA ATTTGATGG TAGTTTCGA GGCTCGGCTC AGGGCATAGA  
67 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300  
68 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA  
69 ATGGCCTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400  
70 TGGAACTATG GGAAATGCAG CTCCACAAACA ACGTATTGTT GCTAACTAG  
71 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAACACCTTT 1500  
72 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GACAGAAATT  
73 TGCTTATGGA ACCTCCTCAA ATTGCCATC CGCTGTATAC AGAAAAAGCG 1600  
74 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA  
75 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTCAA TGTTTCGTT 1700  
76 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)  
77 (start HD-1) CCAACGT TTTCTGGCA GCATCGCAGT 1900  
78 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT  
79 AACAAAATCT ACTAATCTTG GCTCTGGAAAC TTCTGTCGTT AAAGGACCAAG 2000  
80 GATTTACAGG AGGAGATATT CTTGAAAGAA CTTAACCTGG CCAGATTCA  
81 ACCTTAAGAG TAAATATTAC TGCAACCAATT TCACAAAAGAT ATCGGGTAAG 2100  
82 AATTGCTTAC GCTTCTACTA CAAATTTACA ATTCCATACAA TCAATTGACG  
83 GAAGACCTAT TAATCAGGGT AATTTCAGG CAACTATGAG TAGTGGGAGT 2200  
84 AATTTACAGT CCGGAAGCTT TAGGACTGTT GGTTTACTA CTCCGTTAA  
85 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGTCTCAT GTCTTCATT 2300  
86 CAGGCAATGA AGTTTATATA GATCGAAATTG AATTGTTCC GGCAGAAGTA  
87 ACCTTGAGG CAGAATATGA TTAGAAGAG GCACAAAAGG CGGTGAATGA 2400  
88 GCTGTTTACT TCTTCCAAATC AAATGGGTT AAAAACAGAT GTGACGGATT  
89 ATCATATTGA TCAAGTATCC AATTAGTTG AGTGTTCATC AGATGAATT 2500  
90 TGTCGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG  
91 ACTTAGTGT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600  
92 ATAGACAACAT AGACCGTGGC TGGAGAGGGAA GTACGGATAT TACCATCCAA  
93 GGAGSCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700  
94 TGATGAGTGC TATCCAACAT ATTATATCA AAAATAGAT GAGTCGAAAT  
95 TAAAAGCCTA TACCCGTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800  
96 GACTTAGAAA TCTATTAAAT TCGCTACAAT GCAAAACATG AAACAGTAAA  
97 TGTCGCCAGGT ACGGGTTCCT TATGGCCGCT TTCAGCCCCA AGTCCAATCG 2900  
98 GAAAGTGTGG AGAAGCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT  
99 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCC CTCATTGCA 3000  
100 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC  
101 TAGGTGTATG GGTGATCTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
102 CTAGGGAAATC TAGAGTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT  
103 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTAAAAAT 3200  
104 TGGAAATGCGA AACAAATATC GTTATAAAAG AGGCAAAAGA ATCTGTAGAT  
105 GCTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300  
106 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT  
107 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400  
108 GAATAGAAG GGCCTATTTT CACTGCATTG TCCCTATATG ATGCGAGAAA  
109 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500  
110 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCTTGTGTT  
111 CTTCCGGAAT GGGAAAGCAGA AGTGTCAACAA GAAGTTCGTT TCTGTCCGGG 3600  
112 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGAA TATGGAGAAG  
113 GTTGCCTAAC CATTGATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700  
114 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA

M12C1FDF3D2

115 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
116 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC  
117 TATGAAGAAA AATCGTATAAC AGATGGACGA AGAGAGAAATC CTTGTGAATT 3900  
118 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
119 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
120 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAAATTAC TCCTTATGGA  
121 GGAA (end HD-1).

1 48. A process for preparing pesticidal chimeric  
2 toxin EW4 having the following amino acid sequence:

3 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E  
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L  
5 V D I I W G I F G P S Q W D A F P V Q I E Q L I N Q R I E E  
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L L A V  
8 Q N Y Q V P L L S V Y V Q A A N L H U S V L R D V S V F G Q  
9 R W G F D A A T I N S R Y N D L T R U I G N Y T D Y A V R W  
10 Y N T G L E R V W G P D S R D W V R Y N Q F R E L T L T V  
11 L D I V A L F S N Y D S R R Y P I R T V S Q L T R E I Y T N  
12 P V L E N F D G S F R G M A Q R I E Q N I R Q P H L M D I L  
13 N S I T I Y T D V H R G F N Y W S G H Q I T A S P V G F S G  
14 P E F A F F L F G N A G N A A F P V L V S L T G L G I F R T  
15 L S S F P L Y R R I I I L G S G P N N G E L F V L D G T E F S F  
16 A S L T T N L P S T I Y R Q R G T V D S L D V I P P Q D N S  
17 V P P R A G F S H R L S H Y T M L S Q A A G A V Y T L R A Q  
18 R P M F S W I H R S A E F N N I I A S D S I T Q I P A V K G  
19 N F L F N G S V I S G P G F T G G D L V R L N S S G N N I Q  
20 N R G Y I E V P I H F P S T S T R Y R V R V R Y A S V T P I  
21 H L N V N W B N S S I F S N T V P A T A T S L D N L Q S S D  
22 F G Y F E S A N A F T S S L G N I V G V R N F S G T A G V I  
23 I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F  
24 T S T N Q L G L K T N V T D Y H I D Q V S N L V T Y L S D E  
25 F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N  
26 F K D I N R Q F E R G W G G S T G I T I Q G G D D V F K E N  
27 Y V T L S G T F D E C Y F T Y L Y Q K I D E S K L K A F T R  
28 Y Q L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P  
29 G T G S L W F L S A Q S P I G K C G E P N R C A P H L E W N  
30 P D L D C S C R D G E K C A H H S H H F S L D I D V G C T D  
31 L N E D L G V W V I F K I K T Q D G H A R L G N L E F L E E  
32 K P L V G E A L A R V K R A E K K W R D K R E K L E W E T N  
33 I V Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M  
34 I H A A D K R V H S I R E A Y L P E L S V I P G V N A A I F  
35 E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S  
36 C W N V K G H V D V E E Q N N Q R S V L V V P E W E A E E V S  
37 Q E V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H  
38 E I E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y  
39 T V N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S  
40 V Y E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V  
41 G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D  
42 S V E L L L M E E

43 which comprises culturing a prokaryotic microbe  
44 hosting a recombinant DNA transfer vector, denoted  
45 pEW4, comprising DNA having the following nucleotide  
46 sequence or equivalent nucleotide sequences containing  
47 bases whose translated region codes for the same amino  
48 acid sequence:

49 (start HD-1) ATGG ATAACAATCC GAACATCAAT  
50 GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600  
51 TGGAGAAAGA ATAGAAACTG GTTACACCCC AATCGATATT TCCTTGTGCG  
52 TAACGCAATT TCTTTGAGT GAATTTGTTT CCGGGTGTGG ATTTGTGTTA 700  
53 GGAAGTAGTTG ATATAATATG GGGAAATTTT GGTCCCTCTC AATGGGACGC  
54 ATTTCTGTGTA CAAATTGAAC AGTTAATTAA CCAAAGAATA GAAGAATTG 800  
55 CTAGGAACCA AGCCATTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA  
56 ATTTACGCGAG AATCTTTAG AGAGTGGGAA GCGAGATCCTA CTAATCCAGC 900  
57 ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA  
58 CAACCGCTAT TCCTCTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTA 1000  
59 TCAGTATATG TTCAAGCTGC AAATTTACAT TTATCAGTTT TGAGAGATGT  
60 TTCAGTGTGTT GGACAAAGGT GGGGATTTGA TGCCGCGACT ATCAATAGTC 1100  
61 GTTATAATGA TTTAACTAGG CTTATGGCA ACTATACAGA TTATGCTGTG  
62 CGCTGGTACA ATACGGGATT AGAGCGTGTG TGAGGACCGG ATTCTAGAGA 1200  
63 TTGGGTAAGG TATAATCAAT TTAGAAGAGA GCGAACACTT ACTGTATTAG  
64 ATATCGTTGC TCTATTCTCA ATTATGATA GTCGAAGGTA TCCAATTCGA 1300  
65 ACAGTTTCCC AATTAAACAAAG AGAAATTATACGAAACCCAG TATTAGAAAA  
66 TTTTGATGGT AGTTTCTGTG GAATGCGCTCA GAGAATAGAA CAGAATATTA 1400  
67 GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCAT TTATACTGAT  
68 GTGCATAGAG GCTTTAATTA TTGGTCAGGG CATCAAATAA CAGCTTCTCC 1500  
69 TGTTAGGGTTT TCAGGACAG AATTGCGATT CCCTTTATTT GGGAAATGCGG  
70 GGAATGCAGC TCCACCCGTA CTTGTCTCAT TAACTGGTTT GGGGATTTTT 1600  
71 AGAACATTAT CTTCACCTTT ATATAGAAGA ATTATACTTG GTTCAGGGCC  
72 AAATAATCG GAACTGTTG TCCTTGATGG AACGGAGTTT TCTTTGCGCT 1700  
73 CCCTAACGAC GAACTTGCGCT TCCACTATAT ATAGACAAAG GGGTACAGTC  
74 GATTCACTAG ATGTAATACC GCCACAGGAT AATAGTGTAC CACCTCGTGC 1800  
75 GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG  
76 GAGCAGTTA CACCTTGAGA GCTCAACGT (stop HD-1)  
77 (start HD-73) CCT ATGTTCTCTT  
78 GGATACATCG TAGTGCTGAA TTTAATAATA TAATTGCGATC GGATAGTATT 1800  
79 ACTCAAATCC CTGCAGTGAA GGGAAACTTT CTTTTTAATG GTTCTGTAAT  
80 TTCAAGGACCA GGATTTACTG GTGGGGACTT AGTTAGATTA AATAGTAGTG 1900  
81 GAAATAACAT TCAGAAATAGA GGGTATATTG AAGTTCCAAT TCACTTCCCA  
82 TCGACATCTA CCAGATATCG AGTTCGTGTG CGGTATGCTT CTGTAACCCC 2000  
83 GATTCACTC AACGTTAATT GGGGTAATTG ATCCATTGTT TCCAATACAG  
84 TACCAAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTGGT 2100  
85 TATTTGAAA GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG  
86 TGTTAGAAAT TTTAGTGGGA CTGCAGGAGT GATAATAGAC AGATTTGAAT 2200  
87 TTATTCCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG

88 CAGAAGGCAG TGAATGCGCT GTTTACGTCT ACAAAACCAAC TAGGGCTAAA 2300  
 89 AACAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT  
 90 ATTATCGGA TGAATTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400  
 91 GTCAAACATG CGAAGCGACT CAGTGATGAA CGCAATTAC TCCAAGATTC  
 92 AAATTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCGGAAGTA 2500  
 93 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTAAAGA AAATTACGTC  
 94 ACACATATCAG GTACCTTGAA TGAGTGTAT CCAACATATT TGTATCAAAA 2600  
 95 AATCGATGAA TCAAAATTAA AAGCCTTAC CCGTTATCAA TTAAGAGGGT  
 96 ATATCGAAGA TAGTCAAGAC TTAGAAAATCT ATTTAATTGCA CTACAATGCA 2700  
 97 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCCTTAT GGCGCGCTTC  
 98 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCGGCCAC 2800  
 99 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGG TGAGAGAAAAG  
 100 TGTGCCCATC ATTGCGATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900  
 101 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC  
 102 AAGATGGGCA CGCAAGACTA GGGAAATCTAG AGTTTCTCGA AGAGAAACCA 3000  
 103 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAATGGAG  
 104 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAGAGG 3100  
 105 CAAAAGAATC TGAGATGCT TTATTTGTAATCTCGA ACTCTCAATA TGATCAATTAA  
 106 CAAGCGGATA CGAATATTGC CATGATTCAT GCGGCAGATA AACGTGTTCA 3200  
 107 TAGCATTGCA GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA  
 108 ATGCGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTTCAC TGCATTCTCC 3300  
 109 CTATATGATG CGAGAAATGT CATTAAAAAT CGTGTGTTA ATAATGGCTT  
 110 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400  
 111 AACGTTCGGT CCTTGTGTT CCGGAATGGG AAGCAGAAAGT GTCACAAGAA  
 112 GTTCGTGTCG GTCCGGGTCG TGGGTATATC CTTCGTGTCA CAGCGTACAA 3500  
 113 GGAGGGATAT GGAGAAGGTT GCSTAACCAT TCATGAGATC GAGAACAAATA  
 114 CAGACGAACT GAAGTTAGC AACTGCGTAG AAGAGGAAAT CTATCCAAT 3600  
 115 AACACGGTAA CGTGTAAATGA TTATACTGTA AATCAAGAAG AATAACGGAGG  
 116 TGCCTACACT TCTCGTAATC GAGGGATATAA CGAAGCTCCT TCCGTACCAAG 3700  
 117 CTGATTATGC GTCACTGCTAT GAAAGAAAAAT CGTATACAGA TGGACGAAGA  
 118 GAGAACTCCTT GTGAATTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800  
 119 AGTTGGTTAT GTGACAAAAAG ATTAGAATA CTTCCCAGAA ACCGATAAGG  
 120 TATGGATTGA GATTGGAGAA ACGGAAGGGAA CATTATACGT GGACAGCGTG 3900  
 121 GAATTACTCC TTATGGAGAA A (end HD-73).

1           49. A process for preparing pesticidal chimeric  
 2 toxin ACB-1 having the following amino acid sequence:

3           M D N N P M I N E C I P Y N C L S N P E V E V L G G E R I E  
 4           T G Y T P I D I S L S L T Q F I L L S E F V P G A G F V L G L  
 5           V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E  
 6           F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
 7           P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V  
 8           Q N Y Q V P F L L S V Y V Q A A N L H L S V L R D V S V F G Q  
 9           R W S F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
 10          Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V  
 11          L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N  
 12          P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L  
 13          N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G  
 14          P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R



61 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATAACAG 1000  
62 ATTATGCTGT ACGCTGGTAC AATAACGGGAT TAGAACGTGT ATGGGGACCG  
63 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100  
64 AACTGTATTGATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT  
65 ATCCAATTGAAACAGTTTCC CAATTAACAA GAGAAATTAA TACAAACCCA 1200  
66 GTATTAGAAA ATTTGATGG TAGTTTCTGA GGCTCGGCTC AGGGCATAGA  
67 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300  
68 TCTATACGGA TGCTCATAGG GGTTATTATT ATTGGTCAGG GCATCAAATA  
69 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACTT TTCCSCTATA 1400  
70 TGGAACATATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG  
71 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500  
72 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT  
73 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600  
74 GAACGGTAGA TTCGCTGAAT GAAATACCGC CACAGAATAA CAACGTGCCA  
75 CCTAGGCAAG AATTTAGTCA TCGATTAAGC CATGTTCAA TGTTTGTTC 1700  
76 AGGCTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)  
77 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900  
78 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT  
79 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000  
80 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTCA  
81 ACCTTAAGAG TAAATATTAC TGCACCAATT TCAACAAAGAT ATCGGGTAAG 2100  
82 AATTGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG  
83 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200  
84 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTACTA CTCCGTTAA  
85 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300  
86 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAAGAAGTA  
87 ACCTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400  
88 GCTGTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT  
89 ATCATATTGA TCAAGTATCC AATTTAGTTG AATGTTTATC AGATGAATT 2500  
90 TGTCTGGATG AAAAACAAAGA ATTGTCCGAB AAAGTCAAAC ATGCGAAGCG  
91 ACTTACTGAT GAGCGGAATT TACTTCAGA TCCAAACTTC AGAGGGATCA 2600  
92 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA  
93 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700  
94 TGATGAGTGC TATCCAAAGT ATTATATCA AAAAATAGAT GAGTCGAAAT  
95 TAAAAGCTA TACCCGTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800  
96 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA  
97 TGTGCCAGGT ACGGATTCTC TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900  
98 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT  
99 GACTTAGATT GTCGTGTAG GGATGGAGAA AAGTGTGCCA ATCATTGCA 3000  
100 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGAGC  
101 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
102 CTAGGGAATG TAGAGTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT  
103 AGCTCGTGTG AAAAGAGCGG AGAAAAAAATG GAGAGACAAA CGTAAAAAAT 3200  
104 TGGAATGGAA AACAAATATC GTTATATAAG AGGCAAAAGA ATCTGTAGAT  
105 GCTTTATTG TAAACTCTCA ATATGATCAA TTACAAAGCGG ATACGAATAT 3300  
106 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT  
107 ATCTGCGCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGAA 3400  
108 GAATTAGAAG GGCCTATTTT CACTGCATTC TCCCTATATG ATGCGAGAGAA  
109 TGTCAATTAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500  
110 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCCCTGTT  
111 CTTCCGGAAT GGGAAAGCAGA AGTGTACCAA GAAGTGTG TCTGTCCGGG 3600  
112 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAAGGGA TATGGAGAAG

113 GTTGCCTAAC CATTGATGAG ATCGAGAACAA ATACAGACGA ACTGAAGTTT 3700  
114 AGCAACTCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTA  
115 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
116 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC  
117 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900  
118 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
119 AAGAATTAGA ATACTTCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
120 GAAACGGAAG GAACATTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA  
121 GGAA (end HD-1) .

1 50. A process for preparing pesticidal chimeric  
2 toxin SYWI having the following amino acid sequence:

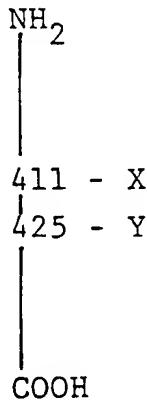
3 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E  
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L  
5 V D I I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E  
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
7 P T N P A L R E E M R I Q F N D M N S A L T T A I F L F A V  
8 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q  
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
10 Y N T G L E R V W G P D S R O W V R Y N Q F R R E L T L T V  
11 L D I V A L F P N Y D S R R Y F I R T V S Q L T R E I Y T N  
12 P V L E N F D G S F R G S A Q G I E G S I R S P H L M D I L  
13 N S I T I Y T D A H K G Y Y W S G H Q I M A S P V G F S G  
14 P E F T F F P L Y G T M S N A A P Q Q R I V A Q L G Q G V Y R  
15 T L S S T L Y R R P E N I G I N N Q Q L S V L D G T E F A Y  
16 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V  
17 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A  
18 P T F S W Q H R S A E F N N I I F S S Q I T Q I P L T K S T  
19 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T  
20 L R V N I T A F L S Q R Y R V R I R Y A S T T N L Q F H T S  
21 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G  
22 F T T P F N F S N G G S S V F T L S A H V F N S G N E V Y I D  
23 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S  
24 S N Q I S L K T D V T D Y H I D Q V S N L V E C L S D E F C  
25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R  
26 G I N R Q L D O R G W R G S T D I T I Q G G G D D V F K E N Y V  
27 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q  
28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T  
29 G S L W F L S A Q S P I G K C G E F N R C A P H L E W N P D  
30 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N  
31 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P  
32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V  
33 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H  
34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E  
35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W  
36 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E  
37 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I  
38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V  
39 N Q E E Y G G A Y T S R N R G Y N E A F S V P A D Y A S V Y  
40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y  
41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V  
42 E L L L M E E

43 which comprises culturing a prokaryotic microbe  
44 hosting a recombinant DNA transfer vector, denoted  
45 pSYW1, comprising DNA having the following nucleotide  
46 sequence or equivalent nucleotide sequences containing  
47 bases whose translated region codes for the same  
48 amino acid sequence:

49 (start HD-73) ATG GATAACAATC 400  
50 CGAACATCAA TGAATGCATT CCTTATAATT STTTAAGTAA CCTGAAAGTA  
51 GAAGTATTAG GTGGAGAAAG AATAGAAAATC GTTACACCC CAATCGATAT 500  
52 TTCCCTTGTG CTAACGCAAT TTCTTTGAG TGAATTGTT CCCGGTGTG  
53 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600  
54 CAATGGGACG CATTCTTGT ACAAAATTGAA CAGTTAATTA ACCAAAGAAAT  
55 AGAAGAATTC GCTAGGAACC AAGCCATTTC TAGATTAGAA GGAACAAAGCA 700  
56 ATCTTATCA AATTACGCA GAATCTTTA GAGAGTGGGA AGCAGATCCT  
57 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800  
58 CAGTGCCTT ACAACCGCTA TTCCCTCTTT TGCAGTTCAA ATTATATCAAG  
59 TTCCCTCTTT ATCAGTATAT GTTCAACCTG CAAATTACA TTTATCAGTT 900  
60 TTGAGAGATG TTTCACTGTT TGGACAAAGG TGGGGATTG ATGCCGCGAC  
61 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATAACAG 1000  
62 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACCGTGT ATGGGGACCG  
63 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTAGAAAGAG ATTAAACACT 1100  
64 AACTGTATTA GATATCGTTG CTGTGTTSCD GAATTATGAT AGTAGAAAGAT  
65 ATCCAATTG AACAGTTTCC CATTAAACAA GAGAAATTAA TACAAACCCCA 1200  
66 GTATTAGAAA ATTTTGATGG TAGTTTCTGA GGCTCGGCTC AGGGCATAGA  
67 AGGAAGSTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300  
68 TCTATACGGA TGCTCATAAA GGGGAATATT ATTGGTCAGG GCATCAAATA  
69 ATGGCTTCTC CTGTTAGGGTT TTGGGGGCCA GAATTCACTT TTCCGCTATA 1400  
70 TGGAACATATG GGAAATGCAG CTCCACAAACA ACGTATTGTT GCTCAACTAG  
71 GTCAGGGCGT GTATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500  
72 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAAATT  
73 TGCTTATGGA ACCTCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600  
74 GAACGGTAGA TTCTGTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA  
75 CCTAGGCAAG GATTAGTCA TCGATTAAGC CATGTTCAA TGTTTCGTT 1700  
76 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)  
77 (start HD-1) CCAACGT TTTCTGGCA GCATCGCAGT 1900  
78 GCTGAATTAA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT  
79 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTGTT AAAGGACCAG 2000  
80 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTTCA  
81 ACCTTAAGAG TAAATATTAC TGCAACATTAA TCACAAAGAT ATCGGGTAAG 2100  
82 AATTGCTAC GCTTCTACTA CAAATTACA ATTCCATACA TCAATTGACG  
83 GAAGACCTAT TAATCAGGGT AATTTCAG GAACTATGAG TAGTGGGAGT 2200  
84 AATTACAGT CGGAAAGCTT TAGGACTGTA GGTTTACTA CTCCGTTAA  
85 CTTTCAAAT GGATCAAGTG TATTACGTT AAGTGCTCAT GTCTTCAATT 2300  
86 TAGGCAATGA AGTTTATATA GATCGAATTG AATTGTTCC GGCAGAAGTA  
87 ACCTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400  
88 GCTGTTACT TCTTCCAATC AAATCGGGTT AAAACAGAT GTGACGGATT  
89 ATCATATTGA TCAAGTATCC AATTAGTTG AGTGTGTTATC AGATGAATT 2500  
90 TGTCTGGATG AAAAACAAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG  
91 ACTTAGTGTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600  
92 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA

93	GGAGGCGATG	ACGTATTCAA	AGAGAATTAC	GTACGCTAT	TGGGTACCTT	2700
94	TGATGAGTGC	TATCCAACGT	ATTTATATCA	AAAAATAGAT	SAGTCGAAAT	
95	TAAAAGCCTA	TACCCGTTAT	CAATTAAGAG	GGTATATCGA	AGATAGTCAA	2800
96	GACTTAGAAA	TCTATTAAAT	TCGCTACAAT	GCAAAACATG	AAACAGTAAA	
97	TGTGCCAGGT	ACGGGTTCCCT	TATGGCCGCT	TTCAGCCCAA	AGTCCAATCG	2900
98	GAAAGTGTGG	AGABCCGAAT	CGATGCGCSC	CACACCTTGA	ATGGAATTCCT	
99	GACTTAGATT	GTTCGTGTAG	GGATGGAGAA	AAGTGTGCC	ATCATTGCGA	3000
100	TCATTTCTCC	TTAGACATTG	ATGTAGGATG	TACAGACTTA	AATGAGGACC	
101	TAGGTGTATG	GGTGATCTT	AAGATTAAGA	CGCAAGATGG	GCACGCAAGA	3100
102	CTAGGGAAATC	TAGAGTTCT	CGAAGAGAAA	CCATTAGTAG	GAGAAGCGCT	
103	AGCTCGTGTG	AAAAGAGCGG	AGAAAAAAATG	GAGAGACAAA	CGTAAAAAT	3200
104	TGGAATGGGA	AACAAATATC	GTTTATAAAG	AGGCAAAAGA	ATCTGTAGAT	
105	GCTTTATTTG	TAACACTCTCA	ATATGATCAA	TTACAAAGCGG	ATACGAATAT	3300
106	TGCCATGATT	CATGCGCAG	ATAAACGTGT	TCATAGCATT	CGAGAAGCTT	
107	ATCTGCCTGA	GCTGTCTGTG	ATTCCGGGTG	TCAATGCGGC	TATTTTTGAA	3400
108	GAATTAGAAG	GGCSTATTTT	CACTGCATTG	TCCCTATATG	ATGCGAGAAA	
109	TGTCATTAAGA	AATGGTGATT	TTAATAATGG	CTTATCCTGC	TGGAACGTGA	3500
110	AAGGGCATGT	AGATGTAGAA	GAACAAAAACA	ACCAACGTTG	GGTCCTTGTG	
111	CTTCCGGAAT	GGGAAGCAGA	AGTGTACCAA	GAAGTTCTG	TCTGTCCGGG	3600
112	TCGTGGCTAT	ATCCTTCGTG	TCACAGCGTA	CAAGGGAGGG	TATGGAGAAG	
113	GTTGCGTAAC	CATTGATGAG	ATCGAGAACG	ATACAGACGA	ACTGAAGTT	3700
114	AGCAACTGCG	TAGAAGAGGA	AATCTATCAA	AATAACACGG	TAACGTGTAA	
115	TGATTATACT	GTAAATCAAG	AAGAAATACGG	AGGTGCGTAC	ACTTCTCGTA	3800
116	ATCGAGGATA	TAACGAAGCT	CCTTCCGTTAC	CAGCTGATT	TGCGTCAGTC	
117	TATGAAGAAA	AATCGTATAC	AGATGGAAGA	AGAGAGAAATC	CTTGTGAATT	3900
118	TAACAGAGGG	TATAGGGATT	ACACGCCACT	ACCAGTTGGT	TATGTGACAA	
119	AAGAATTAGA	ATACTTCCCA	GAAACCGATA	AGGTATGGAT	TGAGATTGGA	4000
120	GAAACGGAAG	GAACATTAT	CGTGGACAGC	GTGGAATTAC	TCCTTATGGA	
121	GGAA (end HD-1).					

51. A chimeric toxin, having the amino acid sequence of toxin EW3, with changes which can be shown schematically as follows:



13 wherein X is one of the 20 common amino acids  
14 except Asp when the amino acid at position 425 is  
15 Gly; Y is one of the 20 common amino acids except  
16 Gly when the amino acid at position 411 is Asp.

1 52. A chimeric toxin, having the amino acid  
2 sequence of toxin EW3, with changes which can be shown  
3 schematically as follows:

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15 wherein X is one of the 20 common amino acids except  
16 Arg when the amino acid at position 311 is Arg and the  
17 amino acid at position 313 is Tyr; Y is one of the 20  
18 common amino acids except Arg when the amino acid at  
19 position 289 is Arg and the amino acid at position 313  
20 is Tyr; and Z is one of the 20 common amino acids  
21 except Tyr when the amino acid at position 289 is  
22 Arg and the amino acid at position 311 is Arg.

1 53. DNA encoding a chimeric toxin as shown in  
2 claim 51.

1 54. DNA encoding a chimeric toxin as shown in  
2 claim 52.

1       55. A recombinant DNA transfer vector comprising  
2       DNA encoding a chimeric toxin as shown in claim 51.

1       56. A recombinant DNA transfer vector comprising  
2       DNA encoding a chimeric toxin as shown in claim 52.

1       57. A chimeric toxin comprising the variable  
2       region or regions of two or more Bacillus toxins.

1       58. A toxin, according to claim 57, wherein the  
2       Bacillus toxins are B. thuringiensis toxins.

1       59. A toxin, according to claim 58, wherein the  
2       B. thuringiensis toxins are B. thuringiensis var.  
3       kurstaki HD-1 toxin and B. thuringiensis var. kurstaki  
4       HD-73 toxin.

1       60. A toxin, according to claim 58, wherein  
2       the B. thuringiensis toxins are encoded by a pesticide-  
3       producing strain of Bacillus thuringiensis, consisting  
4       of B. thuringiensis M-7, B. thuringiensis var. kurstaki,  
5       B. thuringiensis var. finitimus, B. thuringiensis var.  
6       alesti, B. thuringiensis var. sotto, B. thuringiensis  
7       var. dendrolimus, B. thuringiensis var. kenyae, B.  
8       thuringiensis var. galleriae, B. thuringiensis var.  
9       canadensis, B. thuringiensis var. entomocidus, B.  
10      thuringiensis var. subtoxicus, B. thuringiensis var.  
11      aizawai, B. thuringiensis var. morrisoni, B. thuringiensis  
12      var. ostriniae, B. thuringiensis var. tolworthi, B.  
13      thuringiensis var. darmstadiensis, B. thuringiensis  
14      var. toumanoffi, B. thuringiensis var. kyushuensis, B.  
15      thuringiensis var. thompsoni, B. thuringiensis var.  
16      pakistani, B. thuringiensis var. israelensis, B. thurin-  
17      giensis var. indiana, B. thuringiensis var. dakota,

18      B. thuringiensis var. tohokuensis, B. thuringiensis  
19      var. kumanotoensis, B. thuringiensis var. tochigiensis,  
20      B. thuringiensis var. colmeri, B. thuringiensis var.  
21      wuhanensis, B. thuringiensis var. tenebrionis, B.  
22      thuringiensis var. thuringiensis, and other Bacillus  
23      species selected from B. cereus, B. moritai, B.  
24      popilliae, B. lentimorbus, and B. sphaericus.

WHD  
AS